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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:58:19 ; Search time 0.880829 Seconds
(without alignments)
287.324 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFKNIVTPRTTP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pap:
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5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pap:
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pap:
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pap:
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	94	100.0	24	7 US-11-045-024-14523	Sequence 14523, A
2	94	100.0	197	7 US-11-090-878-54	Sequence 54, Appl
3	94	100.0	304	7 US-11-033-039-824	Sequence 824, Appl
4	83.5	88.8	30	7 US-11-106-932-11	Sequence 11, Appl
5	82	87.2	15	7 US-11-150-755-1	Sequence 1, Appl
6	79	84.0	15	7 US-11-150-755-69	Sequence 69, Appl
7	76	80.9	16	7 US-11-045-024-14247	Sequence 14247, A
8	66	70.2	12	7 US-11-033-039-822	Sequence 822, Appl
9	60	63.8	12	6 US-10-893-584-126	Sequence 126, Appl
10	48	51.1	9	7 US-11-033-039-832	Sequence 832, Appl
11	46	48.9	15	7 US-11-106-932-69	Sequence 69, Appl
12	41	43.6	574	7 US-11-072-512-3209	Sequence 3209, Ap
13	39	41.5	337	7 US-11-174-816-43	Sequence 43, Appl
14	39	41.5	337	7 US-11-174-819-11	Sequence 11, Appl
15	39	41.5	1704	7 US-11-075-046-40	Sequence 40, Appl
16	38	40.4	123	7 US-11-195-459-10	Sequence 10, Appl
17	38	40.4	252	7 US-11-012-762-14	Sequence 14, Appl
18	38	40.4	258	6 US-10-467-657-3202	Sequence 3202, Ap
19	38	40.4	318	7 US-11-098-686-10517	Sequence 10517, A
20	38	40.4	376	7 US-11-012-762-10	Sequence 10, Appl
21	38	40.4	376	7 US-11-012-762-16	Sequence 16, Appl
22	38	40.4	376	7 US-11-012-762-18	Sequence 18, Appl
23	38	40.4	376	7 US-11-012-762-20	Sequence 20, Appl
24	38	40.4	376	7 US-11-012-762-24	Sequence 24, Appl
25	38	40.4	376	7 US-11-012-762-40	Sequence 40, Appl

Sequence 70, Appl
Sequence 9210, Ap
Sequence 3879, Ap
Sequence 32, Appl
Sequence 1062, Ap
Sequence 1060, Ap
Sequence 1056, Ap
Sequence 13, Appl
Sequence 1054, Ap
Sequence 1033, Ap
Sequence 1034, Ap
Sequence 10871, A
Sequence 1058, Ap
Sequence 11, Appl
Sequence 10420, A
Sequence 46, Appl
Sequence 6, Appl
Sequence 20, Appl
Sequence 151, Appl
Sequence 2496, Ap

ALIGNMENTS

RESULT 1
US-11-045-024-14523
; Sequence 14523, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14523
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard Peptide 507.02
US-11-045-024-14523

Query Match 100.0%; Score 94; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | |
Db 6 ENPVVHFFKNIIVTRTP 22

RESULT 2

US-11-090-878-54
; Sequence 54, Application US/11090878
; Publication No. US2005024911A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Methods and Reagents for Identifying Compounds for
; TREATING AUTOIMMUNE DISORDERS
; FILE REFERENCE: 98-723-C3
; CURRENT APPLICATION NUMBER: US/11/090,878
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HMBP-21
US-11-090-878-54

Query Match 100.0%; Score 94; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | |
Db 110 ENPVVHFFKNIIVTRTP 126

RESULT 3

US-11-033-039-824
; Sequence 824, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-20170501
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 824
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-824

Query Match 100.0%; Score 94; DB 7; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | |
Db 217 ENPVVHFFKNIIVTRTP 233

RESULT 4

US-11-106-932-11

; Sequence 11, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING

; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-106-932-11

Query Match 88.8%; Score 83.5; DB 7; Length 30;
Best Local Similarity 94.4%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | |
Db 8 ENPVVHFFKNIIVTRTP 25

RESULT 5

US-11-150-755-1
; Sequence 1, Application US/11150755
; Publication No. US20060020109A1
; GENERAL INFORMATION:
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/11/150,755
; CURRENT FILING DATE: 2005-06-10
; PRIOR APPLICATION NUMBER: US/10/056,583
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 85 - 99
; OTHER INFORMATION: Immunodominant peptide of MBP, recognized by
; OTHER INFORMATION: HLA-DR2 haplotype
US-11-150-755-1

Query Match 87.2%; Score 82; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTPR 15
| | | | | | | | | | | | | | | | |
Db 1 ENPVVHFFKNIIVTPR 15

RESULT 6

US-11-150-755-69
; Sequence 69, Application US/11150755
; Publication No. US20060020109A1
; GENERAL INFORMATION:
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha

```

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/11/150,755
; CURRENT FILING DATE: 2005-06-10
; PRIOR APPLICATION NUMBER: US/10/056,583
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-11-150-755-69

Query Match      84.9%; Score 79; DB 7; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.7e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15
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Db 1 ENPVVHFFKNIVTPR 15

RESULT 7
US-11-045-024-14247
; Sequence 14247, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14247
; LENGTH: 16
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14247

Query Match      80.9%; Score 76; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e-07;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VVHFFKNIVTPRTP 17
   |||||:|||||
Db 1 VVHFFKNIVTPRTP 14

RESULT 8
US-11-033-039-822
; Sequence 822, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 822
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-822

Query Match      70.2%; Score 66; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVVHFFKNIVTP 14
   |||||:|||||
Db 1 PVVHFFKNIVTP 12

RESULT 9
US-10-893-584-126
; Sequence 126, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant preproinsulin linker region for calpain, PAP-296
US-10-893-584-126

Query Match      63.8%; Score 60; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00027;

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FFKNIVTPRTP 17
 Db 1 FFKNIVTPRTP 11

RESULT 10

US-11-033-039-832

; Sequence 832, Application US/11033039

; Publication No. US2006002947A1

; GENERAL INFORMATION:

; APPLICANT: HUMPHREYS, ROBERT

; APPLICANT: XU, MINZHEN

; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

; FILE REFERENCE: REH-2017US01

; CURRENT APPLICATION NUMBER: US/11/033,039

; CURRENT FILING DATE: 2005-01-11

; PRIOR APPLICATION NUMBER: 10/245,871

; PRIOR FILING DATE: 2002-09-17

; PRIOR APPLICATION NUMBER: 10/197,000

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: 09/396,813

; PRIOR FILING DATE: 1999-09-14

; NUMBER OF SEQ ID NOS: 1452

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 832

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-033-039-832

Query Match 51.1%; Score 48; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+04;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VHFVKNIPT 13
 Db 1 VHFVKNIPT 9

RESULT 11

US-11-106-932-69

; Sequence 69, Application US/11106932

; Publication No. US20050260697A1

; GENERAL INFORMATION:

; APPLICANT: WANG, KA-WANG KEVIN

; APPLICANT: HAYES, RONALD

; APPLICANT: LIU, MING CHEN

; APPLICANT: OLI, MONIKA

; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN

; FILE REFERENCE: 5853-549-1

; CURRENT APPLICATION NUMBER: US/11/106,932

; CURRENT FILING DATE: 2005-04-15

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 69

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Rattus rattus

US-11-106-932-69

Query Match 48.9%; Score 46; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.07;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFF 8
 Db 8 ENPVVHFF 15

RESULT 12

US-11-072-512-3209

; Sequence 3209, Application US/11072512

; Publication No. US20060029945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUUKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO

; APPLICANT: SEKI, NAOHIKO

; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTOYUKI

; APPLICANT: NAGAHARI, KENJI

; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: 084335-0191

; CURRENT APPLICATION NUMBER: US/11/072,512

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/350,978

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: JP 2001-379298

; PRIOR FILING DATE: 2001-11-05

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3209

; LENGTH: 574

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-072-512-3209

Query Match 43.6%; Score 41; DB 7; Length 574;

Best Local Similarity 47.1%; Pred. No. 28;

Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
 Db 533 ESPRIHPRTPKTPRTP 549

RESULT 13

US-11-174-816-43

; Sequence 43, Application US/11174816

; Publication No. US20060009441A1

; GENERAL INFORMATION:

; APPLICANT: EBELING, MARTIN

; APPLICANT: HOERNER, MARIUS

; APPLICANT: LINDEMANN, LOTHAR

; TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS

; FILE REFERENCE: 22645

; CURRENT APPLICATION NUMBER: US/11/174,816

; CURRENT FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: EP 04103261.6

; PRIOR FILING DATE: 2004-07-08

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 43

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-174-816-43

Query Match 41.5%; Score 39; DB 7; Length 337;

Best Local Similarity 26.7%; Pred. No. 33;

Matches 8; Conservative 5; Mismatches 3; Indels 14; Gaps 1;

REGISTRATION NUMBER: 31,001
REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:57:24 ; Search time 8.69085 Seconds
(without alignments)
817.308 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFFKNIVTPRT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2.6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2.6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2.6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2.6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2.6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	4	US-10-104-973-3
2	94	100.0	17	4	US-10-000-439-13
3	94	100.0	17	4	US-10-362-264-1
4	94	100.0	17	4	US-10-233-892A-2
5	94	100.0	17	5	US-10-482-044-5
6	94	100.0	17	5	US-10-770-712-6
7	94	100.0	19	3	US-09-740-003-2
8	94	100.0	19	3	US-09-768-872-1
9	94	100.0	19	3	US-09-766-378A-32
10	94	100.0	19	4	US-10-239-313A-143
11	94	100.0	19	4	US-10-743-398-2
12	94	100.0	20	3	US-09-766-378A-28
13	94	100.0	20	3	US-09-836-433-30
14	94	100.0	20	3	US-09-859-012-35
15	94	100.0	20	3	US-09-859-012-49
16	94	100.0	21	4	US-10-081-281-33
17	94	100.0	22	5	US-10-492-794-26
18	94	100.0	23	3	US-09-909-460-1
19	94	100.0	23	3	US-09-872-836-1
20	94	100.0	23	3	US-09-906-206A-8
21	94	100.0	23	5	US-10-758-970-1
22	94	100.0	24	4	US-10-149-138-4219
23	94	100.0	24	4	US-10-149-135-2206
24	94	100.0	24	4	US-10-149-138-4219
25	94	100.0	24	4	US-10-149-137A-326
26	94	100.0	24	5	US-10-654-601-2501
27	94	100.0	24	6	US-11-051-411-1220

28 94 100.0 46 3 US-09-813-383-1 Sequence 1, Appli
29 94 100.0 46 3 US-09-813-463A-1 Sequence 1, Appli
30 94 100.0 46 3 US-09-813-463A-1 Sequence 1, Appli
31 94 100.0 123 5 US-10-492-794-115 Sequence 115, App
32 94 100.0 157 4 US-10-425-115-339675 Sequence 339675,
33 94 100.0 169 4 US-10-475-104-32 Sequence 32, Appl
34 94 100.0 169 5 US-10-126-834B-1 Sequence 1, Appli
35 94 100.0 170 4 US-10-015-540-2 Sequence 2, Appli
36 94 100.0 170 4 US-10-199-995-3 Sequence 3, Appli
37 94 100.0 170 5 US-10-773-446-80 Sequence 80, Appl
38 94 100.0 171 2 US-08-484-409-2 Sequence 2, Appli
39 94 100.0 171 3 US-09-989-476-2 Sequence 2, Appli
40 94 100.0 171 3 US-09-947-770-4 Sequence 4, Appli
41 94 100.0 171 3 US-09-893-348-12 Sequence 12, Appl
42 94 100.0 171 3 US-09-218-277-12 Sequence 12, Appl
43 94 100.0 171 4 US-10-104-973-2 Sequence 2, Appli
44 94 100.0 171 4 US-10-000-439-12 Sequence 12, Appl
45 94 100.0 171 4 US-10-270-707-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-104-973-3
; Sequence 3, Application US/10104973
; Publication No. US20020176866A1
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C4
; CURRENT APPLICATION NUMBER: US/10/104,973
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-10-104-973-3

Query Match 100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
|||||
Db 1 ENPVVHFFKNIVTPRT 17

RESULT 2
US-10-000-439-13
; Sequence 13, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-13

Query Match      100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 3
US-10-362-264-1
; Sequence 1, Application US/10362264
; Publication No. US20030191063A1
; GENERAL INFORMATION:
; APPLICANT: Wraith, David
; APPLICANT: Anderton, Stephen
; APPLICANT: Mazza, Graziella
; APPLICANT: Ponsford, Mary
; APPLICANT: Streeter, Heather
; APPLICANT: The University of Bristol
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD
; FILE REFERENCE: 1433.004US1
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03702
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 0020618.5
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 0114547.3
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-264-1

Query Match      100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 4
US-10-233-892A-2
; Sequence 2, Application US/10233892A
; Publication No. US20040043431A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND
; FILE REFERENCE: OTHER DEMYELINATING DISEASES
; FILE REFERENCE: INSMS.001A
; CURRENT APPLICATION NUMBER: US/10/233.892A
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Myelin Binding Protein Sequence 83-89
US-10-233-892A-2

Query Match      100.0%; Score 94; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17

Query Match      100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 5
US-10-482-044-5
; Sequence 5, Application US/10482044
; Publication No. US20040235713A1
; GENERAL INFORMATION:
; APPLICANT: Anna Maria PAPINI et al
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or
; FILE REFERENCE: 2784 PTWO
; CURRENT APPLICATION NUMBER: US/10/482,044
; CURRENT FILING DATE: 2003-12-22
; PRIOR FILING DATE: PCT/EP 02/06767
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: FI2001A000114
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: glycopeptide
; NAME/KEY: CARBOHYD
; LOCATION: (2)..(2)
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl
US-10-482-044-5

Query Match      100.0%; Score 94; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 6
US-10-770-712-6
; Sequence 6, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCI2.008A
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-6

Query Match      100.0%; Score 94; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
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Db      1 ENPVVHFFKNIPTPTP 17
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RESULT 7
US-09-740-003-2
; Sequence 2, Application US/09740003
; Publication No. US20020039582A1
; GENERAL INFORMATION:
; APPLICANT: RAYCHAUDHURI, SYAMAL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: BLACK, AMELIA
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
; FILE REFERENCE: 37003/275802
; CURRENT APPLICATION NUMBER: US/09/740,003
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/024,220
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 08/476,674
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/351,001
; PRIOR FILING DATE: 1994-12-07
; PRIOR APPLICATION NUMBER: 08/919,787
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 07/735,069
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-740-003-2
Query Match      100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIPTPTP 17
Db      2 ENPVVHFFKNIPTPTP 18
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RESULT 8
US-09-768-872-1
; Sequence 1, Application US/09768872
; Patent No. US20020055466A1
; GENERAL INFORMATION:
; APPLICANT: Aharoni, Rina
; APPLICANT: Teitelbaum, Dvora
; APPLICANT: Arnon, Ruth
; APPLICANT: Sela, Michael
; APPLICANT: Fridkis-Hareli, Masha
; APPLICANT: Strominger, Jack
; TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer 1
; FILE REFERENCE: 1662/493762
; CURRENT APPLICATION NUMBER: US/09/768,872
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/093,859
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: US 60/101,825
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: US 60/102,960
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 60/106,350
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 60/108,184
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/123,675

; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (MBP residues 84-102)
US-09-768-872-1
Query Match      100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIPTPTP 17
Db      2 ENPVVHFFKNIPTPTP 18
|||||
US-09-766-378A-32
; Sequence 32, Application US/09766378A
; Patent No. US20020091079A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Acevedo, Jorge
; APPLICANT: Burkhardt, Martin
; APPLICANT: Jiao, Jin-an
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,378A
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/960,190
; FILING DATE: 29-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Corleiss, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-766-378A-32
Query Match      100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ENPVVHFFKNIIVTRTP 17
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Db 2 ENPVVHFFKNIIVTRTP 18
| | | | | | | | | | | | | | | | | | | | | |

RESULT 10

US-10-239-313A-143
; Sequence 143, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-143

Query Match 100.0%; Score 94; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ENPVVHFFKNIIVTRTP 17
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RESULT 11

US-10-743-398-2
; Sequence 2, Application US/10743398
; Publication No. US20040197331A1
; GENERAL INFORMATION:
; APPLICANT: RAYCHAUDHURI, SYAMAL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: BLACK, AMELIA
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
; FILE REFERENCE: 37003/307430
; CURRENT APPLICATION NUMBER: US/10/743,398
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 09/740,003
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/024,220
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 08/476,674
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/351,001
; PRIOR FILING DATE: 1994-12-07
; PRIOR APPLICATION NUMBER: 08/919,787
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 07/735,069
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-743-398-2

Query Match 100.0%; Score 94; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
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Db 2 ENPVVHFFKNIIVTRTP 18
| | | | | | | | | | | | | | | | | | | | | |

RESULT 12

US-09-766-378A-28
; Sequence 28, Application US/09766378A
; Patent No. US20020091079A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Acevedo, Jorge
; APPLICANT: Burkhardt, Martin
; APPLICANT: Jiao, Jing-an
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: DIKE, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/766,378A
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,190
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48002-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-766-378A-28

Query Match 100.0%; Score 94; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | | | | | |
Db 3 ENPVVHFFKNIIVTRTP 19
| | | | | | | | | | | | | | | | | | | | | |

RESULT 13

US-09-836-433-30
 ; Sequence 30, Application US/09836433
 ; Publication No. US20030049797A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuki, Yoshikazu
 ; APPLICANT: Uda, Shigeo
 ; TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
 ; FILE REFERENCE: No. US20030049797A1 Assigned
 ; CURRENT APPLICATION NUMBER: US/09/836,433
 ; CURRENT FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 30
 ; TYPE: PRT
 ; LENGTH: 20
 ; ORGANISM: synthetic construct
 ; ORGANISM: Homo sapiens
 ; US-09-836-433-30

Query Match 100.0%; Score 94; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIPTPT 17
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 DB 3 ENPVVHFFKNIPTPT 19

RESULT 14

US-09-859-012-35
 ; Sequence 35, Application US/09859012
 ; Publication No. US20040253632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RHODE, PETER
 ; APPLICANT: WITTMAN, VAUGHAN
 ; APPLICANT: WEIDANZ, JON A.
 ; APPLICANT: BURKHARDT, MARTIN
 ; APPLICANT: CARD, KIMBERLYN F.
 ; APPLICANT: TAL, RONY
 ; APPLICANT: ACEVEDO, JORGE
 ; APPLICANT: WONG, HING C.
 ; TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS
 ; FILE REFERENCE: 49444 (71758)
 ; CURRENT APPLICATION NUMBER: US/09/859,012
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 60/206,920
 ; PRIOR FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 35
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 ; OTHER INFORMATION: peptide
 ; US-09-859-012-35

Query Match 100.0%; Score 94; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIPTPT 17
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 DB 3 ENPVVHFFKNIPTPT 19

RESULT 15

US-09-859-012-49
 ; Sequence 49, Application US/09859012
 ; Publication No. US20040253632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RHODE, PETER
 ; APPLICANT: WITTMAN, VAUGHAN

; APPLICANT: WEIDANZ, JON A.
 ; APPLICANT: BURKHARDT, MARTIN
 ; APPLICANT: CARD, KIMBERLYN F.
 ; APPLICANT: TAL, RONY
 ; APPLICANT: ACEVEDO, JORGE
 ; APPLICANT: WONG, HING C.
 ; TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS
 ; FILE REFERENCE: 49444 (71758)
 ; CURRENT APPLICATION NUMBER: US/09/859,012
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 60/206,920
 ; PRIOR FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 49
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-859-012-49

Query Match 100.0%; Score 94; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIPTPT 17
 |||||
 DB 3 ENPVVHFFKNIPTPT 19

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:37:34 ; Search time 2.52504 Seconds
(without alignments)
556.619 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFFKNIIVTRTP 17

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	2	US-09-137-759-3
2	94	100.0	17	2	US-09-378-244-3
3	94	100.0	18	1	US-08-468-540B-18
4	94	100.0	19	1	US-08-640-344-2
5	94	100.0	19	1	US-08-468-540B-9
6	94	100.0	19	1	US-08-468-540B-17
7	94	100.0	19	1	US-08-468-540B-24
8	94	100.0	19	2	US-08-297-395-1
9	94	100.0	19	2	US-09-024-220-2
10	94	100.0	19	2	US-08-960-190A-32
11	94	100.0	19	2	US-08-449-728-2
12	94	100.0	19	2	US-09-077-028A-15
13	94	100.0	19	2	US-09-740-003-2
14	94	100.0	20	1	US-08-640-344-1
15	94	100.0	20	1	US-08-640-344-3
16	94	100.0	20	1	US-08-640-344-4
17	94	100.0	20	1	US-08-640-344-5
18	94	100.0	20	1	US-08-640-344-6
19	94	100.0	20	1	US-08-640-344-7
20	94	100.0	20	2	US-08-960-190A-28
21	94	100.0	23	1	US-08-787-547-1
22	94	100.0	24	1	US-08-480-190-46
23	94	100.0	24	1	US-08-488-379-46
24	94	100.0	24	2	US-08-475-399A-46
25	94	100.0	24	2	US-09-239-043D-2501
26	94	100.0	24	2	US-08-077-255A-46
27	94	100.0	24	4	PCT-US93-07545-46

28	94	100.0	40	2	US-08-297-395-2	Sequence 2, Appli
29	94	100.0	168	6	5194425-4	Patent No. 5194425
30	94	100.0	170	1	US-08-227-372-1	Sequence 1, Appli
31	94	100.0	170	1	US-08-327-357A-1	Sequence 1, Appli
32	94	100.0	170	2	US-08-470-397-1	Sequence 1, Appli
33	94	100.0	170	2	US-09-007-520-1	Sequence 3, Appli
34	94	100.0	170	2	US-08-462-351-3	Sequence 1, Appli
35	94	100.0	170	2	US-09-055-263-1	Sequence 3, Appli
36	94	100.0	170	2	US-09-007-520-1	Sequence 1, Appli
37	94	100.0	170	2	US-08-342-408B-2	Sequence 2, Appli
38	94	100.0	170	2	US-09-602-807-3	Sequence 3, Appli
39	94	100.0	170	6	5194425-3	Patent No. 5194425
40	94	100.0	171	1	US-08-781-122-2	Sequence 2, Appli
41	94	100.0	171	2	US-09-137-759-2	Sequence 2, Appli
42	94	100.0	171	2	US-08-953-937-2	Sequence 2, Appli
43	94	100.0	171	2	US-09-378-244-2	Sequence 2, Appli
44	94	100.0	171	2	US-09-989-476-2	Sequence 2, Appli
45	94	100.0	171	2	US-10-270-707-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-137-759-3
; Sequence 3, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C1
; CURRENT APPLICATION NUMBER: US/09/137,759
; CURRENT FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-137-759-3

Query Match 100.0%; Score 94; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
Db 1 ENPVVHFFKNIIVTRTP 17

RESULT 2

US-09-378-244-3
; Sequence 3, Application US/09378244
; Patent No. 6379670
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C2
; CURRENT APPLICATION NUMBER: US/09/378,244
; CURRENT FILING DATE: 1999-08-19

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-378-244-3

Query Match      100.0%; Score 94; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17
Db 1 ENPVVHFFKNIVTPRP 17

RESULT 3
US-08-468-540B-18
; Sequence 18, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-18

Query Match      100.0%; Score 94; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17

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Db 1 ENPVVHFFKNIVTPRP 17

RESULT 4
US-08-640-344-2
; Sequence 2, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT
; APPLICANT: MUKKU, PRABHA
; APPLICANT: DESHPANDE, SHRIRAM
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
; FILING DATE: 30-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 14058-004800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-640-344-2

Query Match      100.0%; Score 94; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17
Db 2 ENPVVHFFKNIVTPRP 18

RESULT 5
US-08-468-540B-9
; Sequence 9, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY

```

COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,540B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jacobs, Seth H
 REGISTRATION NUMBER: 32,140
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-527-7700
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 5858980e
 US-08-468-540B-9

Query Match 100.0%; Score 94; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
 DB 2 ENPVVHFFKNIVTPRTP 18

RESULT 6
 US-08-468-540B-17
 Sequence 17, Application US/08468540B
 Patent No. 5858980
 GENERAL INFORMATION:
 APPLICANT: Weiner, Howard
 APPLICANT: Hafler, David
 APPLICANT: Miller, Ariel
 APPLICANT: Al-Sabbagh, Ahmad
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Darby & Darby P.C.
 STREET: 805 Third Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,540B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jacobs, Seth H

REGISTRATION NUMBER: 32,140
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-527-7700
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 5858980e
 US-08-468-540B-17

Query Match 100.0%; Score 94; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
 DB 2 ENPVVHFFKNIVTPRTP 18

RESULT 7
 US-08-468-540B-24
 Sequence 24, Application US/08468540B
 Patent No. 5858980
 GENERAL INFORMATION:
 APPLICANT: Weiner, Howard
 APPLICANT: Hafler, David
 APPLICANT: Miller, Ariel
 APPLICANT: Al-Sabbagh, Ahmad
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Darby & Darby P.C.
 STREET: 805 Third Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,540B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jacobs, Seth H
 REGISTRATION NUMBER: 32,140
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-527-7700
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 5858980e
 US-08-468-540B-24

Query Match 100.0%; Score 94; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 8e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIPTPT 17
 Db 2 ENPVVHFFKNIPTPT 18

RESULT 8

US-08-297-395-1
 ; Sequence 1, Application US/08297395A
 ; Patent No. 6039947
 ; GENERAL INFORMATION:
 ; APPLICANT: Howard L. Weiner
 ; APPLICANT: David A. Hafler
 ; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
 ; TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
 ; FILE REFERENCE: 1010/05723US3
 ; CURRENT APPLICATION NUMBER: US/08/297,395A
 ; CURRENT FILING DATE: 1994-08-11
 ; EARLIER APPLICATION NUMBER: 08/059,189
 ; EARLIER FILING DATE: 1993-05-06
 ; EARLIER APPLICATION NUMBER: 07/502,559
 ; EARLIER FILING DATE: 1990-03-30
 ; EARLIER APPLICATION NUMBER: PCT/US88/02139
 ; EARLIER FILING DATE: 1988-06-24
 ; EARLIER APPLICATION NUMBER: 07/065,734
 ; EARLIER FILING DATE: 1987-06-24
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-08-297-395-1

Query Match 100.0%; Score 94; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIPTPT 17
 Db 2 ENPVVHFFKNIPTPT 18

RESULT 9

US-09-024-220-2
 ; Sequence 2, Application US/09024220
 ; Patent No. 6197311
 ; GENERAL INFORMATION:
 ; APPLICANT: RAYCHAUDHURI, Syamal
 ; RASTETTER, William H.
 ; BLACK, Amelia
 ; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE
 ; RESPONSES
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/024,220
 ; FILING DATE: 17-Feb-1998
 ; CLASSIFICATION: <Unknown>
 ; 24-JUL-1999

25-JUL-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/476,674
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 07/919,787
 ; FILING DATE: 24-JUL-1992
 ; APPLICATION NUMBER: US 07/735,069
 ; FILING DATE: 25-JUL-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-149
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-024-220-2
 Query Match 100.0%; Score 94; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ENPVVHFFKNIPTPT 17
 Db 2 ENPVVHFFKNIPTPT 18
 RESULT 10
 US-08-960-190A-32
 ; Sequence 32, Application US/08960190A
 ; Patent No. 6232445
 ; GENERAL INFORMATION:
 ; APPLICANT: Rhode, Peter R.
 ; APPLICANT: Acevedo, Jorge
 ; APPLICANT: Burkhardt, Martin
 ; APPLICANT: Jiao, Jin-an
 ; APPLICANT: Wong, Hing C.
 ; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
 ; METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: usa
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/960,190A
 ; FILING DATE: 29-OCT-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Corless, Peter F
 ; REGISTRATION NUMBER: 33,860
 ; REFERENCE/DOCKET NUMBER: 48002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440

TELEX:
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-960-190A-32

Query Match 100.0%; Score 94; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
 Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 11
 US-08-449-728-2
 Sequence 2, Application US/08449728
 Patent No. 6270769
 GENERAL INFORMATION:
 APPLICANT: SYAMAL RAYCHAUDHURI
 APPLICANT: WILLIAM H. RASTETTER
 TITLE OF INVENTION: INDUCTION OF CYTOTOXIC
 TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 611 West Sixth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90017

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 SOFTWARE: WordPerfect (Version 5.0)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,728
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/735,069
 FILING DATE: 25-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 194/160
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-449-728-2

Query Match 100.0%; Score 94; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
 Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 12
 US-09-077-028A-15
 Sequence 15, Application US/09077028A
 Patent No. 6531133
 GENERAL INFORMATION:
 APPLICANT: HAYA LOREBERBOUM-GALSKI
 APPLICANT: IDA STEINBERGER
 APPLICANT: EVELINE BERAUD
 APPLICANT: IRINA MARIANOVSKY
 APPLICANT: SHAI YARKONI
 TITLE OF INVENTION: PSEUDOMONAS EXOTOXIN-MYELIN BASIC PROTEIN CHIMERIC
 FILE REFERENCE: LOREBERBOUM-1
 CURRENT APPLICATION NUMBER: US/09/077,028A
 PRIOR FILING DATE: 1998-05-18
 PRIOR APPLICATION NUMBER: IL116044
 PRIOR FILING DATE: 1995-11-17
 PRIOR APPLICATION NUMBER: IL116559
 PRIOR FILING DATE: 1995-12-26
 PRIOR APPLICATION NUMBER: PCT/IL96/00151
 PRIOR FILING DATE: 1996-11-17
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 15
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-077-028A-15

Query Match 100.0%; Score 94; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
 Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 13
 US-09-740-003-2
 Sequence 2, Application US/09740003
 Patent No. 6733763
 GENERAL INFORMATION:
 APPLICANT: RAYCHAUDHURI, SYAMAL
 APPLICANT: RASTETTER, WILLIAM H.
 APPLICANT: BLACK, AMELIA
 TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
 FILE REFERENCE: 37003/275802
 CURRENT APPLICATION NUMBER: US/09/740,003
 CURRENT FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: 09/024,220
 PRIOR FILING DATE: 1998-02-17
 PRIOR APPLICATION NUMBER: 08/476,674
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/351,001
 PRIOR FILING DATE: 1994-12-07
 PRIOR APPLICATION NUMBER: 08/919,787
 PRIOR FILING DATE: 1997-08-29
 PRIOR APPLICATION NUMBER: 07/735,069
 PRIOR FILING DATE: 1991-07-25
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: peptide
 US-09-740-003-2

Query Match 100.0%; Score 94; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
Db 2 ENPVVHFFKNIIVTRTP 18

RESULT 14

US-08-640-344-1
; Sequence 1, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT
; APPLICANT: MUKKU, PRABHA
; APPLICANT: DESHPANDE, SHRIKANT
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
; FILING DATE: 30-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 14058-004800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-640-344-1

Query Match 100.0%; Score 94; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
Db 3 ENPVVHFFKNIIVTRTP 19

RESULT 15

US-08-640-344-3
; Sequence 3, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT
; APPLICANT: MUKKU, PRABHA
; APPLICANT: DESHPANDE, SHRIKANT
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO

; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
; FILING DATE: 30-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 14058-004800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-640-344-3

Query Match 100.0%; Score 94; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
Db 3 ENPVVHFFKNIIVTRTP 19

Search completed: February 22, 2006, 21:39:50
Job time : 3.52504 secs

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:24 ; Search time 11.304 Seconds
(without alignments)
1061.041 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	74	2 Q6AI64 HUMAN	Q6ai64 homo sapien
2	94	100.0	128	2 Q505J1 RAT	Q505j1 rattus norv
3	94	100.0	150	2 Q5NVG4 PONPY	Q5nvq4 pongo pygma
4	94	100.0	154	2 Q542T4 MOUSE	Q542t4 mus musculu
5	94	100.0	158	2 Q8R4K6 RAT	Q8r4k6 rattus norv
6	94	100.0	160	2 Q6FI04 HUMAN	Q6fi04 homo sapien
7	94	100.0	160	2 Q6FH37 HUMAN	Q6fh37 homo sapien
8	94	100.0	160	2 Q5R7J4 PONPY	Q5r7j4 pongo pygma
9	94	100.0	167	1 MBP_CAVPO	P25188 cavia porce
10	94	100.0	168	1 MBP_RABIT	P25274 oryctolagus
11	94	100.0	169	1 MBP_BOVIN	P02887 bos taurus
12	94	100.0	171	1 MBP_PANTR	P06906 pan troglod
13	94	100.0	171	1 MBP_PIG	P81558 sus scrofa
14	94	100.0	171	2 Q5R618 PONPY	Q5r618 pongo pygma
15	94	100.0	173	2 Q6J2R3 PIG	Q6j2r3 sus scrofa
16	94	100.0	180	2 Q6PK23 HUMAN	Q6pk23 homo sapien
17	94	100.0	194	1 MBP_RAT	P02888 rattus norv
18	94	100.0	203	2 Q65ZS4 HUMAN	Q65z84 homo sapien
19	94	100.0	250	1 MBP_MOUSE	P04370 mus musculu
20	94	100.0	304	1 MBP_HUMAN	P02686 homo sapien
21	87	92.6	173	1 MBP_CHICK	P15720 gallus gall
22	87	92.6	178	2 Q511E1 GECJA	Q511e1 gekko japon
23	87	92.6	178	2 Q569T2_XENLA	Q569t2 xenopus lae
24	84	89.4	175	1 MBP_XENLA	P87346 xenopus lae
25	78	83.0	172	1 MBP_HORSE	P83487 equus cabal
26	65	69.1	217	2 Q4RF19 TETNG	Q4rf19 tetraodon n
27	61	64.9	154	1 MBP_RAJER	Q91325 raja erinac
28	61	64.9	154	1 MBP_SQUAC	Q91439 squalus aca
29	60	63.8	128	1 MBP_CAROB	P98190 carcharhinu
30	53	56.4	154	1 MBP_HETFR	P20939 heterodonu
31	52	55.3	88	2 Q512C7_BRARE	Q512c7 brachydanio

32	51	54.3	516	2 QSWTL4 LEGPL	Q5wtl4 legionella
33	49.5	52.7	668	2 Q86I29 DICDI	Q86i29 dictyosteli
34	49	52.1	516	2 Q5X1V3 LEGPA	Q5x1v3 legionella
35	47	50.0	300	2 Q833W5_ENTFA	Q833w5 enterococcu
36	47	50.0	516	2 Q5ZSD2 LEGPH	Q5zsd2 legionella
37	47	50.0	669	2 Q6D8B7 ERWCT	Q6d8b7 erwinia car
38	46	48.9	233	2 Q6J37 CAEBR	Q6j37 caenorhabdi
39	46	48.9	287	2 Q58M89_9CAUD	Q58m89 cyanophage
40	46	48.9	439	2 Q4ZST7_PSESY	Q4zst7 pseudomonas
41	46	48.9	440	2 Q881D3_PSESM	Q881d3 pseudomonas
42	46	48.9	888	2 Q4QAJ6_LEIMA	Q4qaj6 leishmania
43	46	48.9	1529	2 Q7ZX12_XENLA	Q7zx12 xenopus lae
44	45	47.9	308	1 Y1128 METJA	Q58528 methanococc
45	45	47.9	315	2 Q4H5F9_9DEIO	Q4h5f9 deinococcus

ALIGNMENTS

RESULT 1
Q6AI64 HUMAN
ID Q6AI64_HUMAN PRELIMINARY; PRT; 74 AA.
AC Q6AI64;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686I0845 (Fragment).
GN Name=DKFZp686I0845;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Amygdala;
RG The German cDNA Consortium;
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR627018; CAH10359.1; -; mRNA.
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_MBP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KW Hypothetical protein.
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 8265 MW; ACFE96ACBE9AE551 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
|||||
DB 41 ENPVVHFFKNIVTPRTP 57

RESULT 2
Q505J1 RAT
ID Q505J1_RAT PRELIMINARY; PRT; 128 AA.
AC Q505J1;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Myelin basic protein.
GN Name=Mbp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vellanton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Brain;
 RC NIH MGC Project;
 RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC094522; AAH94522.1; -, mRNA.
 DR InterPro: IPR000548; Myelin BP.
 DR Pfam: PF01669; Myelin MBP; I.
 DR PRINTS; PR00212; MYELINMBP.
 DR PRODOM; PD004542; Myelin BP; 1.
 DR PROSITE; PS00569; MYELIN MBP; 1.
 SQ SEQUENCE 128 AA; 14211 MW; 2DAF033C19CF111C CRC64;

Query Match 100.0%; Score 94; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0;

QY 1 ENPVVHFFKNIVTPRT 17
 |||||
 DB 81 ENPVVHFFKNIVTPRT 97
 |||||

RESULT 3
 Q5NVG4 PONPY PRELIMINARY; PRT; 150 AA.
 AC Q5NVG4
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Hypothetical protein DKFZp459G2410.
 GN Name=DKFZp459G2410;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Cortex;
 RC The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR926072; CAI29699.1; -, mRNA.
 DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
 DR InterPro; IPR000548; Myelin BP.
 DR Pfam; PF01669; Myelin MBP; 1.
 DR PRINTS; PR00212; MYELINMBP.
 DR PRODOM; PD004542; Myelin BP; 1.

DR PROSITE; PS00569; MYELIN MBP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 150 AA; 16277 MW; AF41CDB96D8FD01 CRC64;
 Query Match 100.0%; Score 94; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
 |||||
 DB 63 ENPVVHFFKNIVTPRT 79
 |||||

RESULT 4
 Q542T4 MOUSE PRELIMINARY; PRT; 154 AA.
 ID Q542T4
 AC Q542T4
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Adult male spinal cord cDNA, RIKEN full-length enriched library,
 DE clone:A330075E24 product:myelin basic protein, full insert
 DE sequence.
 DE Name=Mbp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Koshikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takehashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AK079621; BAC37705.1; -; mRNA.
DR MGI; MG1:96925; Mdp.
DR GO; GO:0042552; P:myelination; IDA.
SQ SEQUENCE 154 AA; 17225 MW; 00F1F10EFC90421B CRC64;

Query Match 100.0%; Score 94; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
|||||
DB 107 ENPVVHFFKNIVTPRTP 123

RESULT 5

Q8R4K6 RAT PRELIMINARY; PRT; 158 AA.
AC Q8R4K6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myelin basic protein.
GN Name=Mbp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22941125; PubMed=14580679; DOI=10.1016/j.bbaexp.2003.08.010;
RA Mathews L., Blair G.E.;
RT "Identification and characterisation of a cDNA encoding a 17-kDa
RT isoform of rat myelin basic protein.";
RL Biochim. Biophys. Acta 1630:47-53(2003).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Sprague-Dawley;
RA Mathews L.M., Blair G.E.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF439750; AAL84189.1; -; mRNA.
DR GO; GO:0015911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 158 AA; 17240 MW; 3256580242ECC3E1 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
|||||
DB 81 ENPVVHFFKNIVTPRTP 97

RESULT 6

Q6FI04 HUMAN PRELIMINARY; PRT; 160 AA.
AC Q6FI04;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MBP protein.
GN Name=MBP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoondinya M., Schick M., Eisenstein S.,
RA Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR536534; CAG38771.1; -; mRNA.
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 160 AA; 17347 MW; 0107AAD6053CD876 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 84 ENPVVHFFKNIIVTRTP 100

RESULT 7
 Q6FH37 HUMAN
 ID Q6FH37 HUMAN PRELIMINARY; PRT; 160 AA.
 AC Q6FH37;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE MBP protein (Fragment).
 GN Name=MBP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., LaBaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR541919; CAG46717.1; -, mRNA.
 FT NON TER 160
 SQ SEQUENCE 160 AA; 17343 MW; 0107AAD603FCD876 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 84 ENPVVHFFKNIIVTRTP 100

RESULT 8
 Q5R7J4 PONPY
 ID Q5R7J4 PONPY PRELIMINARY; PRT; 160 AA.
 AC Q5R7J4;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein DKFZp459C0311.
 GN Name=DKFZp459C0311;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Pobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR860121; CAH92286.1; -, mRNA.
 GO GO:0019911; F:structural constituent of myelin sheath; IEA.
 DR InterPro; IPR000548; Myelin BP.
 DR Pfam; PF01669; Myelin MBP; I.
 DR PRINTS; PR00212; MYELINMBP.
 DR ProDom; PD004542; Myelin BP; 1.
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 160 AA; 17317 MW; 1A0601CCB257D9C6 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 84 ENPVVHFFKNIIVTRTP 100

RESULT 9
 MBP_CAVPO
 ID MBP_CAVPO STANDARD; PRT; 167 AA.
 AC P25I88;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Myelin basic protein (MBP).
 GN Name=MBP;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Mystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA MEDLINE=84215086; PubMed=6202840;
 RA Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;
 RT "Sequence of guinea pig myelin basic protein.";
 RL J. Neurochem. 43:100-105 (1984).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 7-156.
 RC STRAIN=Hartley; TISSUE=Spinal cord;
 RA Kim G., Tanuma N., Matsumoto Y.;
 RT "DNA vaccination using Guinea pig myelin basic protein coding region
 in experimental autoimmune encephalomyelitis.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PROTEIN SEQUENCE OF 45-87.
 RA Shapira R., McKneally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640 (1971).
 RN [4]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=76025020; PubMed=51849;
 RA Deibler G.E., Martenson R.E., Kramer A.J., Kies M.W.;
 RT "The contribution of phosphorylation and loss of COOH-terminal
 arginine to the microheterogeneity of myelin basic protein.";
 RL J. Biol. Chem. 250:7931-7938 (1975).
 CC -I- FUNCTION: Is, with PLP, the most abundant protein component of the
 myelin membrane in the CNS. Has a role in both the formation and
 stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 function in the assembly of an optimized, biochemically functional
 myelin membrane (By similarity).
 CC -I- SUBUNIT: Homodimer (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -I- TISSUE SPECIFICITY: Found in both the central and the peripheral
 nervous system.
 CC -I- PTM: At least 5 charge isomers; C1 (the most cationic, least
 modified, and most abundant form), C2, C3, C4 and C5 (the least
 cationic form); are produced as a result of optional
 posttranslational modifications such as phosphorylation of serine
 or threonine residues, deamidation of glutamine or asparagine
 residues, citrullination and methylation of arginine residues. C1
 and C2 are unphosphorylated, C3 and C4 are monophosphorylated and
 C5 is phosphorylated at two positions.
 CC -I- SIMILARITY: Belongs to the myelin basic protein family.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not

Qy 1 ENPVVHFFKNIIVTRTP 17
 Db 81 ENPVVHFFKNIIVTRTP 97
 RESULT 11
 MBP_BOVIN STANDARD; PRT; 169 AA.
 AC P02687; Q9BGM8; Q9TS63; Q9TS66;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-SEP-2005 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule
 DE stabilizing protein).
 GN Name=MBP;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RX MEDLINE=72007306; PubMed=5096093;
 RA Eylar E.H., Brostoff S.W., Hashim G., Caccam J., Burnett P.;
 RT "Basic A1 protein of the myelin membrane. The complete amino acid
 RT sequence.";
 RL J. Biol. Chem. 246:5770-5784 (1971).
 RN [2]
 RN SEQUENCE REVISION.
 RX MEDLINE=74070688; PubMed=4129204;
 RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";
 RL J. Biol. Chem. 249:559-567 (1974).
 RN [3]
 RN NUCLEOTIDE SEQUENCE OF 4-56.
 RA Pietrowski D., Medugorac I., Foerster M.;
 RT "A new MBP allele in Bos taurus is characterized by BseNI PCR-RFLP.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN PROTEIN SEQUENCE OF 43-87.
 RA Shapira R., McKeally S.S., Chou F.C.-H., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640 (1971).
 RN [5]
 RN PROTEIN SEQUENCE OF 38-58 AND 119-141.
 RC TISSUE=Brain;
 RX MEDLINE=93003019; PubMed=1382581;
 RA Pirollet F., Derancourt J., Haiech J., Job D., Margolis R.L.;
 RT "Ca(2+)-calmodulin regulated effectors of microtubule stability in
 RT bovine brain.";
 RL Biochemistry 31:8849-8855 (1992).
 RN [6]
 RN PROTEIN SEQUENCE OF 30-42; 74-89 AND 114-129.
 RX MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;
 RA Prasad K., Barouch W., Martin B.M., Greene L.E., Eisenberg E.;
 RT "Purification of a new clathrin assembly protein from bovine brain
 RT coated vesicles and its identification as myelin basic protein.";
 RL J. Biol. Chem. 270:30551-30556 (1995).
 RN [7]
 RN SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.
 RX MEDLINE=70178977; PubMed=5442707;
 RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;
 RT "Experimental allergic encephalomyelitis: synthesis of disease-
 RT inducing site of the basic protein.";
 RL Science 168:1220-1223 (1970).
 RN [8]
 RN METHYLATION.
 RX MEDLINE=71153946; PubMed=4994464;
 RA Brostoff S.W., Eylar E.H.;
 RT "Localization of methylated arginine in the A1 protein from myelin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769 (1971).
 RN [9]
 RN POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=76167591; PubMed=57115;
 RA Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.;
 RT "Basis of microheterogeneity of myelin basic protein.";
 RL J. Biol. Chem. 251:2671-2679 (1976).
 RN [10]
 RN PROTEIN SEQUENCE OF 97-104, AND PHOSPHORYLATION SITE THR-97.
 RX MEDLINE=91060584; PubMed=1700979;
 RA Erickson A.K., Payne D.M., Martino P.A., Rosomando A.J.,
 RA Shabanowitz J., Weber M.J., Hunt D.F., Scurgill T.W.;
 RT "Identification by mass spectrometry of threonine 97 in bovine myelin
 RT basic protein as a specific phosphorylation site for mitogen-activated
 RT protein kinase.";
 RL J. Biol. Chem. 265:19728-19735 (1990).
 RN [11]
 RN POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=98153125; PubMed=9485392; DOI=10.1021/bi972347t;
 RA Zand R., Li M.X., Jin X., Lubman D.;
 RT "Determination of the sites of posttranslational modifications in the
 RT charge isomers of bovine myelin basic protein by capillary
 RT electrophoresis-mass spectroscopy.";
 RL Biochemistry 37:2441-2449 (1998).
 RN [12]
 RN DIMERIZATION.
 RX MEDLINE=80198320; PubMed=6155143;
 RA Smith R.;
 RT "Sedimentation analysis of the self-association of bovine myelin basic
 RT protein.";
 RL Biochemistry 19:1826-1831 (1980).
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
 CC myelin membrane in the CNS. Has a role in both the formation and
 CC stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 CC function in the assembly of an optimized, biochemically functional
 CC myelin membrane (By similarity).
 CC -1- SUBUNIT: Homodimer; self-associates in the presence of lysolipid.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral
 CC nervous system.
 CC -1- PTM: At least 6 charge isomers; C1 (the most cationic and least
 CC modified form), C2, C3, C4, C5 and C6 (the least cationic form);
 CC are produced as a result of optional posttranslational
 CC modifications, such as phosphorylation of serine or threonine
 CC residues, deamidation of glutamine or asparagine residues,
 CC citrullination and methylation of arginine residues.
 CC -1- SIMILARITY: Belongs to the myelin basic protein family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL: AF226693; AAK00645.1; -; mRNA.
 CC PIR: A92089; MBBOR.
 CC HSP: P02686; IQCU.
 CC InterPro: IPR000548; Myelin_BP.
 CC PANTHER: PTHR11429; Myelin_BP; 1.
 CC Pfam: PF01669; Myelin_MBP; 1.
 CC PRINTS: PR00212; MYELINMBP.
 CC ProDom: PD004542; Myelin_BP; 1.
 CC PROSITE: PS00569; MYELIN_MBP; 1.
 CC Acetylation; Autoimmune encephalomyelitis; Citrullination;
 CC Direct protein sequencing; Methylation; Myelin; Phosphorylation;
 CC Structural protein.
 CC REGION 43 87 Induces experimental autoimmune
 CC encephalomyelitis (EAE) 1.
 CC REGION 114 122 Induces experimental autoimmune
 CC encephalomyelitis (EAE) 2.
 CC MOD_RES 1 1 N-acetylalanine.
 CC MOD_RES 7 7 Phosphoserine (in C5 and C6).
 CC MOD_RES 10 10 Phosphoserine (By similarity).

```

FT MOD_RES 23 23 Citrulline (By similarity).
FT MOD_RES 29 29 Citrulline (By similarity).
FT MOD_RES 54 54 Phosphoserine (in C4, C5 and C6).
FT MOD_RES 69 69 Phosphoserine (By similarity).
FT MOD_RES 97 97 Phosphothreonine (by MAPK) (in C3, C4, C5
and C6).
FT MOD_RES 102 102 Deamidated glutamine (in form C5).
FT MOD_RES 106 106 Omega-N-methylarginine (alternate).
FT MOD_RES 106 106 Symmetric dimethylarginine (alternate).
FT MOD_RES 114 114 Phosphoserine (By similarity).
FT MOD_RES 129 129 Citrulline (By similarity).
FT MOD_RES 146 146 Deamidated glutamine (in form C2).
FT MOD_RES 158 158 Citrulline (By similarity).
FT MOD_RES 160 160 Phosphoserine (in C4 and C6).
FT MOD_RES 164 164 Phosphoserine (in C3, C5 and C6).
FT MOD_RES 169 169 Citrulline (Probable).
SQ SEQUENCE 169 AA; 18323 MW; 8E1157B7A1978484 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
Db 82 ENPVVHFFKNIVTPRTP 98

RESULT 12
MBP_PANTH
ID MBP_PANTH STANDARD; PRT; 171 AA.
AC P06306;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Myelin basic protein (MBP).
GN Name=MBP;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP PRELIMINARY PROTEIN SEQUENCE.
RX MEDLINE=76009821; PubMed=51459; DOI=10.1016/0024-3205(75)90506-8;
RA Westall F.C., Thompson M., Kalter S.S.;
RT "The proposed sequence of the encephalitogenic protein from chimpanzee
brain".
RL Life Sci. 17:219-223(1975).
CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -!- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -!- SIMILARITY: Belongs to the myelin basic protein family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A03139; MRC2B.
DR HSP; P02686; IQCL.
DR InterPro; IPR000548; Myelin_BP.
DR PANTHER; PTHR11429; Myelin_BP; 1.

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DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PD00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KW Acetylation; Autoimmune encephalomyelitis; Citrullination;
Direct protein sequencing; Methylation; Myelin; Phosphorylation;
KW Structural protein.
FT MOD_RES 1 1 N-acetylalanine.
FT MOD_RES 7 7 Phosphoserine (By similarity).
FT MOD_RES 12 12 Phosphoserine (By similarity).
FT MOD_RES 25 25 Citrulline (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 56 56 Phosphoserine (By similarity).
FT MOD_RES 71 71 Phosphoserine (By similarity).
FT MOD_RES 98 98 Phosphothreonine (By similarity).
FT MOD_RES 103 103 Deamidated glutamine (partial) (By
similarity).
FT MOD_RES 107 107 Omega-N-methylated arginine.
FT MOD_RES 115 115 Phosphoserine (By similarity).
FT MOD_RES 122 122 Citrulline (By similarity).
FT MOD_RES 130 130 Citrulline (By similarity).
FT MOD_RES 148 148 Deamidated glutamine (partial) (By
similarity).
FT MOD_RES 160 160 Citrulline (By similarity).
FT MOD_RES 162 162 Phosphoserine (By similarity).
FT MOD_RES 166 166 Phosphoserine (By similarity).
FT MOD_RES 171 171 Citrulline (By similarity).
SQ SEQUENCE 171 AA; 18560 MW; E9FED59DE6933293 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
Db 83 ENPVVHFFKNIVTPRTP 99

RESULT 13
MBP_PIG
ID MBP_PIG STANDARD; PRT; 171 AA.
AC P81558; P98189;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Myelin basic protein (MBP).
GN Name=MBP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP PROTEIN SEQUENCE, AND METHYLATION OF ARG-107.
RC TISSUE=Brain;
RX MEDLINE=85056964; PubMed=2578056;
RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
RT "Amino acid sequence of porcine myelin basic protein.";
RL J. Neurochem. 44:134-142(1985).
RN [2]
RP ERRATUM.
RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
RL J. Neurochem. 44:1663-1663(1985).
CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -!- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as

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phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.
-1- SIMILARITY: Belongs to the myelin basic protein family.

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PR; A61640; MBPGB.
HSP; P02686; IQCL.
InterPro: IPR000548; Myelin_BP.
PANTHER; PTHR11429; Myelin_BP; 1.
Pfam; PF01669; Myelin_MBP; 1.
PRINTS; PR00212; MYELINMBP.
ProDom; PD004542; Myelin_BP; 1.
PROSITE; PS00569; MYELIN_MBP; 1.
Myelin; Phosphorylation; Structural protein.
Acetylation; Citrullination; Direct protein sequencing; Methylation;
FT MOD_RES 1 1 N-acetylalanine.
FT MOD_RES 7 7 Phosphoserine (By similarity).
FT MOD_RES 12 12 Phosphoserine (By similarity).
FT MOD_RES 25 25 Citrulline (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 55 55 Phosphoserine (By similarity).
FT MOD_RES 70 70 Phosphoserine (By similarity).
FT MOD_RES 98 98 Phosphothreonine (By similarity).
FT MOD_RES 103 103 Deamidated glutamine (partial) (By similarity).
FT MOD_RES 107 107 Omega-N-methylarginine (alternate).
FT MOD_RES 107 107 Symmetric dimethylarginine (alternate).
FT MOD_RES 115 115 Phosphoserine (By similarity).
FT MOD_RES 130 130 Citrulline (By similarity).
FT MOD_RES 148 148 Deamidated glutamine (partial) (By similarity).
FT MOD_RES 160 160 Citrulline (By similarity).
FT MOD_RES 162 162 Phosphoserine (By similarity).
FT MOD_RES 166 166 Phosphoserine (By similarity).
FT MOD_RES 171 171 Citrulline (By similarity).
SEQUENCE 171 AA; 18487 MW; 287ADF2F24028D9 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
Db 83 ENPVVHFFKNIVTPRT 99

RESULT 14
Q5R618_PONV PRELIMINARY; PRT; 171 AA.
AC Q5R618;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459C0215 (Hypothetical protein DKFZp459P2220).
GN Name=DKFZp459C0215; Synonyms=DKFZp459P2220;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo
OC NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RG Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR860682; CAH92798.1; -; mRNA.
DR EMBL; CR926007; CAI2645.1; -; mRNA.
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KW Hypothetical protein.
SQ SEQUENCE 171 AA; 18565 MW; F8B56E03D6305540 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
Db 84 ENPVVHFFKNIVTPRT 100

RESULT 15
Q6J2R3_PIG PRELIMINARY; PRT; 173 AA.
ID Q6J2R3_PIG PRELIMINARY;
AC Q6J2R3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Myelin basic protein.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15717131; DOI=10.1111/j.1365-2052.2005.01236.x;
RA Kim J.G., Noneman D., Vallet J.L., Rohrer G.A., Christenson R.K.;
RT "Linkage mapping of the porcine myelin basic protein gene to chromosome 1."
RL Anim. Genet. 36:163-164 (2005).
DR EMBL; AV603684; AAT28338.1; -; mRNA.
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP; 1.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 173 AA; 18731 MW; 66B4D016E66081AA CRC64;

Query Match 100.0%; Score 94; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
Db 85 ENPVVHFFKNIVTPRT 101

Search completed: February 22, 2006, 21:37:14
Job time : 13.304 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:31:15 ; Search time 1.7323 Seconds
(without alignments)
944.229 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFKNIVTPRP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	94	100.0	128	1 MBRTS	myelin basic prote
2	94	100.0	167	2 A37246	myelin basic prote
3	94	100.0	169	1 MB80B	myelin basic prote
4	94	100.0	171	1 MB80B	myelin basic prote
5	94	100.0	171	1 MB80B	myelin basic prote
6	94	100.0	197	1 MB80B	myelin basic prote
7	94	100.0	328	1 MB80B	golli-myelin basic
8	87	92.6	174	2 S08535	myelin basic prote
9	60	63.8	128	2 A60215	myelin basic prote
10	53	56.4	155	2 B32999	myelin basic prote
11	45	47.9	308	2 G64440	hypothetical prote
12	44	46.8	329	2 A57246	beta-tectorin prec
13	44	46.8	639	2 T46577	arylsulfatase (EC
14	43	45.7	14	2 S12904	protein kinase (EC
15	43	45.7	85	2 C89965	conserved hypothet
16	43	45.7	134	2 T28704	hypothetical prote
17	43	45.7	395	2 H72222	conserved hypothet
18	43	45.7	672	2 A11183	transcription regu
19	43	45.7	1124	2 B84742	probable receptor-
20	42	44.7	435	2 AB3076	glutamine synthet
21	42	44.7	435	2 G98210	glutamine synthet
22	42	44.7	435	2 JC1301	glutamate-ammonia
23	42	44.7	672	2 AG1541	Similar to transcr
24	42	44.7	891	2 T40137	hypothetical serin
25	41	43.6	48	2 D82534	hypothetical prote
26	41	43.6	332	2 E70384	biotin synthase (E
27	41	43.6	480	2 A12308	cytochrome b ubiqu
28	41	43.6	646	2 A11174	internalin, probab
29	41	43.6	690	2 E84945	glycine-tRNA ligas

ALIGNMENTS

RESULT 1

MBRTS

myelin basic protein S - rat
N:Alternate names: small myelin basic protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Apr-1984 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: B24351; A90275; A94243; A21062; A03142
R:Schaich, M.; Budzinski, R.M.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 825-834, 1986
A:Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the
A:Reference number: A24351; MUID:87026249; PMID:2429678
A:Accession: B24351
A:Molecule type: mRNA
A:Residues: 1-128 <SCH>
A:Cross-references: UNIPROT:P02688; UNIPARC:UPI0000163B8F; EMBL:M25889; NID:g205321; PIR:
R:Dunkley, P.R.; Carnegie, P.R.
Biochem. J. 141, 243-255, 1974
A:Title: Amino acid sequence of the smaller basic protein from rat brain myelin.
A:Reference number: A90275; MUID:75127359; PMID:4141893
A:Accession: A90275
A:Molecule type: protein
A:Residues: 2-128 <DUN>
A:Cross-references: UNIPARC:UPI000002ADB4
A:Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in th
R:McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKneally, S.; Shapira, R.
Science 179, 478-480, 1973
A:Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogen
A:Reference number: A94243; MUID:73180720; PMID:4122324
A:Accession: A94243
A:Molecule type: protein
A:Residues: 46-86 <MCP>
A:Cross-references: UNIPARC:UPI00001740CC
A:Note: the sequence reported for this encephalitogenic peptide differs from that shown
R:Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.E.
Cell 34, 799-806, 1983
A:Title: Characterization of cloned cDNA representing rat myelin basic protein: absence
A:Reference number: A21062; MUID:84026484; PMID:6194889
A:Accession: A21062
A:Molecule type: mRNA
A:Residues: 1-124, 'I', 126-128 <ROA>
A:Cross-references: UNIPARC:UPI000002E780
A:Experimental source: strain Sprague-Dawley
C:Superfamily: myelin basic protein
C:Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy
F:2-128/Product: myelin basic protein S #status experimental <NAT>
F:2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #stat
F:105/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 128;

Best Local Similarity 100.0%; Pred. No. 9.6e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTRTP 17
 |||||
 Db 81 ENPVVHFFKNIVTRTP 97

RESULT 2

A37246
 myelin basic protein - guinea pig
 N;Alternate names: myelin A1 protein
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 31-Jul-1991 #sequence revision 31-Jul-1991 #text_change 09-Jul-2004
 C;Accession: A37246; C92087; A03140
 R;Deibler, G.E.; Martenson, R.B.; Krutzsch, H.C.; Kies, M.W.
 J. Neurochem. 43, 100-105, 1984
 A;Title: Sequence of guinea pig myelin basic protein.
 A;Reference number: A37246; MUID:84215086; PMID:6202840
 A;Accession: A37246
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-167 <DBI>
 A;Cross-references: UNIPROT:P25188; UNIPARC:UPI000012BD39
 R;Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971
 A;Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
 A;Reference number: A92087
 A;Accession: C92087
 A;Molecule type: protein
 A;Residues: 45-87 <SHA>
 A;Cross-references: UNIPARC:UPI000017780D
 C;Superfamily: myelin basic protein
 C;Keywords: myelin

Query Match 100.0%; Score 94; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTRTP 17
 |||||
 Db 82 ENPVVHFFKNIVTRTP 98

RESULT 3

MBB0B
 myelin basic protein - bovine
 N;Alternate names: myelin A1 protein
 N;Contains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 18-Dec-1981 #sequence revision 18-Dec-1981 #text change 09-Jul-2004
 C;Accession: A92089; A92160; A92087; S54343; A61641; B61641; A03140
 R;Eylar, E.H.; Brostoff, S.; Hasham, G.; Caccam, J.; Burnett, P.
 J. Biol. Chem. 246, 5770-5784, 1971
 A;Title: Basic A1 protein of the myelin membrane. The complete amino acid sequence.
 A;Reference number: A92089; MUID:72007306; PMID:5096093
 A;Accession: A92089
 A;Molecule type: protein
 A;Residues: 1,'S',2-169 <EYL>
 A;Cross-references: UNIPROT:P02687; UNIPARC:UPI0000148533
 R;Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
 J. Biol. Chem. 249, 559-567, 1974
 A;Title: Specific cleavage of the A1 protein from myelin with cathepsin D.
 A;Reference number: A92160; MUID:74070688; PMID:4129204
 A;Accession: A92160
 A;Molecule type: protein
 A;Residues: 1-169 <BRO>
 A;Cross-references: UNIPARC:UPI000012BD38
 R;Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971
 A;Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
 A;Reference number: A92087
 A;Accession: A92087
 A;Molecule type: protein
 A;Residues: 43-87 <SHA>

A;Cross-references: UNIPARC:UPI00001740BD
 R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
 Biochem. J. 306, 551-555, 1995
 A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in gli
 A;Reference number: S54343; MUID:95194333; PMID:7887910
 A;Accession: S54343
 A;Molecule type: protein
 A;Residues: 74-75,'HG',78-82,'D',84-88,'105','X',107-108,'X',110-114,'X',116-119 <OKA>
 A;Cross-references: UNIPARC:UPI00001740BE; UNIPARC:UPI00001740BF
 R;Takamatsu, K.; Tatamoto, K.
 Neurochem. Res. 17, 239-246, 1992
 A;Title: Isolation and characterization of two novel peptide amides originating from my
 A;Reference number: A61641; MUID:92319189; PMID:1377792
 A;Accession: A61641
 A;Molecule type: protein
 A;Residues: 1-12 <TAK>
 A;Cross-references: UNIPARC:UPI00001740C0
 A;Accession: B61641
 A;Molecule type: protein
 A;Residues: 1-16 <TA2>
 A;Cross-references: UNIPARC:UPI00001740C0
 A;Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymat
 R;Brostoff, S.; Eylar, E.H.
 Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971
 A;Title: Localization of methylated arginine in the A1 protein from myelin.
 A;Reference number: A93777; MUID:71153946; PMID:4994464
 A;Contents: annotation
 A;Note: Arg-106 is modified to monomethylarginine and dimethylarginine
 R;Eylar, E.H.; Caccam, J.; Jackson, J.J.; Westall, F.C.; Robinson, A.B.
 Science 168, 1220-1223, 1970
 A;Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site of
 A;Reference number: A94241; MUID:70178977; PMID:5442707
 A;Contents: annotation
 A;Note: the region including residues 114-122 induces experimental allergic encephalomy
 C;Superfamily: myelin basic protein
 C;Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune enceph
 F;1-16/Product: myelin basic protein #status experimental <MAT>
 F;1-16/Product: myelin peptide amide-16 #status experimental <PA16>
 F;1-12/Product: myelin peptide amide-12 #status experimental <PA12>
 F;1/Modified site: acetylated amino end (Ala) #status experimental
 F;12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide am
 F;16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide am
 F;106/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 169;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTRTP 17
 |||||
 Db 82 ENPVVHFFKNIVTRTP 98

RESULT 4
 MBC2B
 myelin basic protein - chimpanzee (tentative sequence)
 N;Alternate names: MBP
 C;Species: Pan troglodytes (chimpanzee)
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C;Accession: A03139
 R;Westall, F.C.; Thompson, M.; Kalter, S.S.
 Life Sci. 17, 219-223, 1975
 A;Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
 A;Reference number: A03139; MUID:76009821; PMID:51459
 A;Accession: A03139
 A;Molecule type: protein
 A;Residues: 1-171 <WES>
 A;Cross-references: UNIPROT:P06906; UNIPARC:UPI000012BD3D
 C;Comment: This protein may function in maintaining the proper structure of myelin.
 C;Superfamily: myelin basic protein
 C;Keywords: blocked amino end; methylated amino acid; myelin; structural protein
 F;1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
 F;107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 83 ENPVVHFFKNIVTPRTP 99

RESULT 5
 MBPGB
 myelin basic protein - pig (tentative sequence)
 N:Alternate names: myelin A1 protein
 N:Contains: myelin basic protein amide 14
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 09-Jul-2004
 C:Accession: A61640; A36245
 R:Kira, J.; Deibler, G.E.; Krutzsch, H.C.; Martenson, R.E.
 J. Neurochem. 44, 134-142, 1985
 A:Title: Amino acid sequence of porcine myelin basic protein.
 A:Reference number: A61640; MUID:85056964; PMID:2578056
 A:Accession: A61640
 A:Molecule type: protein
 A:Residues: 1-171 <KIR>
 A:Cross-references: UNIPROT:P81558; UNIPARC:UPI000012ED3E
 A>Note: some peptides were ordered by homology
 R:Takamatsu, K.; Tatamoto, K.
 Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990
 A:Title: Isolation and characterization of a novel peptide amide from porcine brain.
 A:Reference number: A36245; MUID:91058553; PMID:1700904
 A:Accession: A36245
 A:Molecule type: protein
 A:Residues: 1-14 <TAK>
 A:Cross-references: UNIPARC:UPI00001740C2
 A>Note: the sequence in the abstract is inconsistent with that in figure 3 in having Glu
 C:Superfamily: myelin basic protein
 C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis
 F:1-171/Product: myelin basic protein #status experimental <MAT>
 F:1-14/Product: myelin peptide amide-14 #status experimental <PA12>
 F:14/Modified site: acetylated amino end (Ala) #status experimental
 F:14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amide)
 F:107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg) (amide in mature form myelin peptide amide)

Query Match 100.0%; Score 94; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 83 ENPVVHFFKNIVTPRTP 99

RESULT 6
 MBHUB
 myelin basic protein [validated] - human
 N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein precursor, 5K splice form
 C:Species: Homo sapiens (man)
 C:Date: 18-Dec-1981 #sequence_revision 25-Aug-1995 #text_change 09-Jul-2004
 C:Accession: S10482; A94106; A90256; JH0802; A60862; A61420; A33273; I54219; I56
 R:Streicher, R.; Scofield, W.
 Biol. Chem. Hoppe-Seyler 370, 503-510, 1989
 A:Title: The organization of the human myelin basic protein gene. Comparison with the mouse gene.
 A:Reference number: S10482; MUID:89302693; PMID:2472816
 A:Accession: S10482
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-197 <STR>
 A:Cross-references: UNIPROT:P02686; UNIPARC:UPI000002ADA4; EMBL:X17286; NID:g34490; PIDN:R1Kam012; J. De Feira, F.; Puckett, C.; Lazzarini, R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986

A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.
 A:Reference number: A94106; MUID:86259714; PMID:2425357
 A:Accession: A94106
 A:Molecule type: mRNA
 A:Residues: 1-59,86-197 <KAM>
 A:Cross-references: UNIPARC:UPI000002ADA6; GB:M13577; NID:g187408; PIDN:AAAS9562.1; PID:A94106
 A>Note: 18.5K splice form
 A:Accession: B94106
 A:Molecule type: mRNA
 A:Residues: 1-197 <KA2>
 A:Cross-references: UNIPARC:UPI000002ADA4
 A>Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form
 A>Note: a 17.2K splice form is also described
 A>Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K splice form
 R:Carnegie, P.R.
 Biochem. J. 123, 57-67, 1971
 A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.
 A:Reference number: A90256; MUID:72066400; PMID:4108501
 A:Accession: A90256
 A:Molecule type: protein
 A:Residues: 2-59,86-197 <CAR>
 A:Cross-references: UNIPARC:UPI0000113626
 R:Proost, P.; Van Damme, J.; Opdenakker, G.
 Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993
 A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin bas
 A:Reference number: JH0802; MUID:93282820; PMID:7685161
 A:Accession: JH0802
 A:Molecule type: protein
 A:Residues: 2-59,86-137 <PRO>
 A:Cross-references: UNIPARC:UPI0000113626
 A:Experimental source: brain
 R:Scoble, H.A.; Whitaker, J.N.; Biemann, K.
 J. Neurochem. 47, 614-616, 1986
 A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44 a
 A:Reference number: A60862; MUID:86280476; PMID:2426402
 A:Accession: A60862
 A:Molecule type: protein
 A:Residues: 2-45,117-197 <SCO>
 A:Cross-references: UNIPARC:UPI00001740B8; UNIPARC:UPI00001740B9
 A>Note: evidence for acetylated amino end
 R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.
 J. Biol. Chem. 259, 5028-5031, 1984
 A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined;
 A:Reference number: A61420; MUID:84185608; PMID:6201481
 A:Accession: A61420
 A:Molecule type: protein
 A:Residues: 46-59,86-116 <GIB>
 A:Cross-references: UNIPARC:UPI00001740BA
 R:Wood, D.D.; Moscarello, M.A.
 J. Biol. Chem. 264, 5121-5127, 1989
 A:Title: The isolation, characterization, and lipid-aggregating properties of a citrullin
 A:Reference number: A33273; MUID:89174797; PMID:2466844
 A:Accession: A33273
 A:Molecule type: protein
 A:Residues: 15-25,'X',27-31,'X',33-59,86-148,'X',150-156,'X',158-185,'X',187-196,'X' <NR
 A:Cross-references: UNIPARC:UPI00001740BB
 R:Baldwin, G.S.; Carnegie, P.R.
 Biochem. J. 123, 69-74, 1971
 A:Title: Isolation and partial characterization of methylated arginines from the enceph
 A:Reference number: A30257; MUID:72066401; PMID:5128665
 A:Contents: annotation; methylation
 A>Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the appo
 R:Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.
 J. Immunol. 105, 1223-1230, 1970
 A:Reference number: A92806; MUID:71088405; PMID:4099924
 A:Contents: annotation
 A>Note: a region including residues 139-149 induces experimental autoimmune encephalomyel
 R:Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.
 Genomics 6, 16-22, 1990
 A:Title: Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a new form of
 A:Reference number: I54219; MUID:90152679; PMID:1689270
 A:Accession: I54219

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-59 <RES>
A;Cross-references: UNIPARC:UPI000016AD10; GB:M63599; NID:g187402; PIDN:AAA59560.1; PID:
R;Roth, H.J.; Kronquist, K.E.; Kerlero de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 17, 321-328, 1987
A;Title: Evidence for the expression of four myelin basic protein variants in the develop
A;Reference number: I56567; MUID:87311781; PMID:2442403
A;Accession: I56567
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-132,144-197 <RE2>
A;Cross-references: UNIPARC:UPI000002ADAS; GB:M30516; NID:g187410; PIDN:AAA59563.1; PID:
A;Accession: I73634
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-197 <RE3>
A;Cross-references: UNIPARC:UPI000002ADAA; GB:M30515; NID:g187412; PIDN:AAA59564.1; PID:
R;Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 16, 227-238, 1986
A;Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin
A;Reference number: I56565; MUID:86308101; PMID:2427738
A;Accession: I56565
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-59,86-133,145-197 <RE4>
A;Cross-references: UNIPARC:UPI000002ADAY; GB:M30047; NID:g187400; PIDN:AAA59559.1; PID:
R;Boulias, C.; Pang, H.; Mastrionardi, F.; Moscarello, M.A.
Arch. Biochem. Biophys. 322, 174-182, 1995
A;Title: The isolation and characterization of four myelin basic proteins from the unbo
A;Reference number: S66383; MUID:96004793; PMID:7574672
A;Accession: S66383
A;Molecule type: protein
A;Residues: 23-25,'X',27-39 <BOU>
A;Cross-references: UNIPARC:UPI00001740BC
C;Comment: Four alternatively spliced forms of myelin basic protein have been observed,
C;Genetics:
A;Gene: GDB:MBP
A;Cross-references: GDB:I119379; OMIM:159430
A;Map position: 18q22-18qter
A;Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
C;Function:
A;Description: probably helps maintain myelin structure
C;Superfamily: myelin basic protein
C;Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimm
F;2-197/Product: myelin basic protein, 21.5K splice form #status predicted <MAT1>
F;2-132,144-197/Product: myelin basic protein, 20.2K splice form #status predicted <MAT2
F;2-59,86-197/Product: myelin basic protein, 18.5K splice form #status experimental <MAT
F;2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experiment
F;134/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg) (

Query Match 100.0%; Score 94; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENPVVHFPPKNIIVTRTP 17
Dbb 110 ENPVVHFPPKNIIVTRTP 126
RESULT 7
MBMSB
N;Alternate names: golli-mbp precursor - mouse
N;Contains: myelin basic protein
C;Species: Mus musculus (house mouse)
C;Date: 17-Mar-1987 #sequence_revision 07-Oct-1994 #text change 09-Jul-2004
C;Accession: A45421; B45421; A90867; A90867; A26591; A60920; I48407; I58996; I54
R;Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry,
J. Biol. Chem. 268, 4930-4938, 1993
A;Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that e

A;Reference number: A45421; MUID:93186801; PMID:7680345
A;Accession: A45421
A;Molecule type: mRNA
A;Residues: 1-190;217-276;316-328 <CAM1>
A;Cross-references: UNIPROT:P04370; UNIPARC:UPI00001740C3; UNIPARC:UPI00001740C4; UNIPAR
A;Experimental source: clone J37
A;Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified
A;Accession: B45421
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-191,'SSEP' <CAM2>
A;Cross-references: UNIPARC:UPI0000004029; GB:L07508; NID:g193586; PIDN:AAA37721.1; PID
A;Experimental source: clone BG21
A;Note: sequence extracted from NCBI backbone (NCBIN:126700, NCBI:P:126715)
R;de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzarin
Cell 43, 721-727, 1985
A;Title: Alternative splicing accounts for the four forms of myelin basic protein.
A;Reference number: A90875; MUID:86079555; PMID:2416470
A;Accession: A90875
A;Molecule type: mRNA
A;Residues: 134-328 <DEF>
A;Cross-references: UNIPARC:UPI000002ADAA9; GB:L00404; GB:M11669; NID:g199060; PIDN:AAA
A;Experimental source: 21.5K
R;Takahashi, N.; Roach, A.; Teplov, D.B.; Prusiner, S.B.; Hood, L.
Cell 42, 139-148, 1985
A;Title: Cloning and characterization of the myelin basic protein gene from mouse: one
A;Reference number: A90867; MUID:85254913; PMID:2410136
A;Accession: A90867
A;Molecule type: DNA
A;Residues: 134-190;217-328 <PAK>
A;Cross-references: UNIPARC:UPI00001740C6; UNIPARC:UPI00001740C7; GB:M11533; NID:g19904
A;Experimental source: 18.5K
R;Newman, S.; Kitamura, K.; Campagnoni, A.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987
A;Title: Identification of a cDNA coding for a fifth form of myelin basic protein in mo
A;Reference number: A94188; MUID:87118269; PMID:2433693
A;Accession: A26591
A;Molecule type: mRNA
A;Residues: 134-274;316-328 <NEW1>
A;Cross-references: UNIPARC:UPI00001740C5; UNIPARC:UPI00001740C8; GB:M15060; NID:g19904
A;Experimental source: clone M722; splice form 17.22K
A;Accession: B26591
A;Molecule type: mRNA
A;Residues: 134-190;217-263;275-328 <NEW2>
A;Cross-references: UNIPARC:UPI00001740C6; UNIPARC:UPI00001740C9; UNIPARC:UPI00001740CA
A;Experimental source: clone M78; splice form 17.24K
R;Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V.W
J. Neurochem. 54, 2032-2041, 1990
A;Title: Expression of a novel transcript of the myelin basic protein gene.
A;Reference number: A60920; MUID:90250449; PMID:1692584
A;Accession: A60920
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 134-190;217-274;316-328 <KIT>
A;Cross-references: UNIPARC:UPI00001740C5; UNIPARC:UPI00001740C6; UNIPARC:UPI00001740C3
A;Experimental source: M41; splice form 14K
R;Grima, B.; Zelenika, D.; Pessac, B.
J. Neurochem. 59, 2318-2323, 1992
A;Title: A novel transcript overlapping the myelin basic protein gene.
A;Reference number: I48407; MUID:93057537; PMID:1279125
A;Accession: I48407
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-191,'SSEP' <GRI>
A;Cross-references: UNIPARC:UPI0000004029; EMBL:X67319; NID:g51332; PIDN:CAA47733.1; PI
A;Note: submitted to the EMBL Data Library, July 1992
R;Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
A;Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin ba
A;Reference number: I58996; MUID:84119431; PMID:6198644
A;Accession: I58996
A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 219-248 <ZEL>
A:Cross-references: UNIPARC:UPI000016CED2; GB:K00989; NID:gl199037; PIDN:AAA39495.1; PID:
R.Miura, M.; Tamura, T.
Gene 75, 31-38, 1989
A:Title: The promoter elements of the mouse myelin basic protein gene function efficient
A:Reference number: I54033; MUID:89252919; PMID:2470651
A:Accession: I54033
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 134-157 <MTU>
A:Cross-references: UNIPARC:UPI000016CED5; GB:M24410; NID:gl199052; PIDN:AAA39498.1; PID:
R.Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.
EMBO J. 7, 77-83, 1988
A:Title: Gene organization and transcription of duplicated MBP genes of myelin deficient
A:Reference number: I53256; MUID:88196094; PMID:2452084
A:Accession: I53256
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 217-229, 'HN', 232-250 <OKA>
A:Cross-references: UNIPARC:UPI000016CED6; GB:M36275; NID:gl199069; PIDN:AAA39504.1; PID:
A.Note: hypothetical translation of the reversed and complementary sequence to that show
C:Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and
C:Genetics:
A:Gene: Golli-mbp; shi-mld
A:Introns: 190/3; 250/3; 262/3; 273/3; 314/3
A:Function:
A:Description: probably helps maintain myelin structure
C:Superfamily: myelin basic protein
C:Keywords: alternative splicing; myelin; structural protein
F:130-217, 276-316-328/Product: Golli-mbp protein (clone J37) #status predicted <MAL>
F:134-328/Product: myelin basic protein, splice form 21.5K #status predicted <MAT>
F:134-274, 316-328/Product: myelin basic protein, splice form 17K-a #status predicted <MA
F:134-190, 217-328/Product: myelin basic protein, splice form 18.5K #status predicted <MA
F:134-190, 217-263, 275-328/Product: myelin basic protein, splice form 17K-b #status predi
F:134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predict

Query Match 100.0%; Score 94; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
|||||
DB 240 ENPVVHFFKNIVTPRTP 256
|||||

RESULT 8
S08535
myelin basic protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S08535
R:Zopf, D.; Sontag, V.; Betz, H.; Gundelfinger, E.D.
Glia 2, 241-249, 1989
A:Title: Developmental accumulation and heterogeneity of myelin basic protein transcript
A:Reference number: S08535; MUID:89358239; PMID:2475444
A:Accession: S08535
A:Molecule type: mRNA
A:Residues: 1-174 <ZOP>
A:Cross-references: UNIPROT:P15720; UNIPARC:UPI0000171364; EMBL:X17103; NID:g63594; PIDN
C:Superfamily: myelin basic protein

Query Match 92.6%; Score 87; DB 2; Length 174;
Best Local Similarity 88.2%; Pred. No. 2.2e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
:|||||
DB 82 DNPVVHFFKNIVSPRTP 98
:|||||

RESULT 9
A60215

A:Molecule type: mRNA
A:Residues: 219-248 <ZEL>
A:Cross-references: UNIPARC:UPI000016CED2; GB:K00989; NID:gl199037; PIDN:AAA39495.1; PID:
R.Miura, M.; Tamura, T.
Gene 75, 31-38, 1989
A:Title: The promoter elements of the mouse myelin basic protein gene function efficient
A:Reference number: I54033; MUID:89252919; PMID:2470651
A:Accession: I54033
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 134-157 <MTU>
A:Cross-references: UNIPARC:UPI000016CED5; GB:M24410; NID:gl199052; PIDN:AAA39498.1; PID:
R.Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.
EMBO J. 7, 77-83, 1988
A:Title: Gene organization and transcription of duplicated MBP genes of myelin deficient
A:Reference number: I53256; MUID:88196094; PMID:2452084
A:Accession: I53256
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 217-229, 'HN', 232-250 <OKA>
A:Cross-references: UNIPARC:UPI000016CED6; GB:M36275; NID:gl199069; PIDN:AAA39504.1; PID:
A.Note: hypothetical translation of the reversed and complementary sequence to that show
C:Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and
C:Genetics:
A:Gene: Golli-mbp; shi-mld
A:Introns: 190/3; 250/3; 262/3; 273/3; 314/3
A:Function:
A:Description: probably helps maintain myelin structure
C:Superfamily: myelin basic protein
C:Keywords: alternative splicing; myelin; structural protein
F:130-217, 276-316-328/Product: Golli-mbp protein (clone J37) #status predicted <MAL>
F:134-328/Product: myelin basic protein, splice form 21.5K #status predicted <MAT>
F:134-274, 316-328/Product: myelin basic protein, splice form 17K-a #status predicted <MA
F:134-190, 217-328/Product: myelin basic protein, splice form 18.5K #status predicted <MA
F:134-190, 217-263, 275-328/Product: myelin basic protein, splice form 17K-b #status predi
F:134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predict

Query Match 100.0%; Score 94; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
|||||
DB 240 ENPVVHFFKNIVTPRTP 256
|||||

RESULT 8
S08535
myelin basic protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S08535
R:Zopf, D.; Sontag, V.; Betz, H.; Gundelfinger, E.D.
Glia 2, 241-249, 1989
A:Title: Developmental accumulation and heterogeneity of myelin basic protein transcript
A:Reference number: S08535; MUID:89358239; PMID:2475444
A:Accession: S08535
A:Molecule type: mRNA
A:Residues: 1-174 <ZOP>
A:Cross-references: UNIPROT:P15720; UNIPARC:UPI0000171364; EMBL:X17103; NID:g63594; PIDN
C:Superfamily: myelin basic protein

Query Match 92.6%; Score 87; DB 2; Length 174;
Best Local Similarity 88.2%; Pred. No. 2.2e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
:|||||
DB 82 DNPVVHFFKNIVSPRTP 98
:|||||

RESULT 9
A60215

myelin basic protein - dusky shark (fragments)
C:Species: Carcharhinus obscurus (dusky shark)
C:Date: 10-Nov-1992 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: A60215
R:Milne, T.J.; Atkins, A.R.; Warren, J.A.; Auton, W.P.; Smith, R.
J. Neurochem. 55, 950-955, 1990
A:Title: Shark myelin basic protein: amino acid sequence, secondary structure, and self
A:Reference number: A60215; MUID:90347482; PMID:1696624
A:Accession: A60215
A:Molecule type: protein
A:Residues: 1-128 <MI>
A:Cross-references: UNIPROT:P98190; UNIPARC:UPI00000FDESC
A:Note: the source was designated as Carcharhinus obscurus (whaler shark)
C:Superfamily: myelin basic protein

Query Match 63.8%; Score 60; DB 2; Length 128;
Best Local Similarity 52.9%; Pred. No. 0.0065;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
::|||||
DB 46 DSAVVHFFKNMSPKAP 62
::|||||

RESULT 10
B32999
myelin basic protein - horn shark
C:Species: Heterodontus francisci (horn shark)
C:Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 09-Jul-2004
C:Accession: B32999
R:Saavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood,
J. Mol. Evol. 29, 149-156, 1989
A:Title: The myelin proteins of the shark brain are similar to the myelin proteins of t
A:Reference number: A32999; MUID:90040744; PMID:2478717
A:Accession: B32999
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <SAA>
A:Cross-references: UNIPROT:P20939; UNIPARC:UPI00001713F7; GB:X17664; NID:g63974; PIDN:
C:Superfamily: myelin basic protein

Query Match 56.4%; Score 53; DB 2; Length 155;
Best Local Similarity 53.3%; Pred. No. 0.13;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15
::|||||
DB 72 DSAVVHFFKNMSPK 86
::|||||

RESULT 11
G64440
hypothetical protein MJ1128 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: G64440
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
ron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64440
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-308 <BUL>
A:Cross-references: UNIPROT:Q58528; UNIPARC:UPI0000065082; GB:U67555; GB:L77117; NID:gl
C:Genetics:
A:Map position: REV1069975-1069049
A:Start codon: GTG
C:Superfamily: hypothetical protein MJ1128

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Query Match      47.9%; Score 45; DB 2; Length 308;
Best Local Similarity 70.0%; Pred. No. 6.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ENPVVHFFKN 10
    ||||: ||||
Db 35 ENPVIQYFKN 44

RESULT 12
A57246
beta-tectorin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57246
R;Killick, R.; Legan, P.K.; Malenczak, C.; Richardson, G.P.
J. Cell Biol. 129, 535-547, 1995
A;Title: Molecular cloning of chick beta-tectorin, an extracellular matrix molecule of
A;Reference number: A57246; MUID:95238547; PMID:7721949
A;Accession: A57246
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-329 <KIL>
A;Cross-references: UNIPROT:P54097; UNIPARC:UPI0000136B89; GB:L38519; NID:G602439; PIDN:
C;Keywords: extracellular matrix; membrane protein; phosphatidylinositol linkage

Query Match      46.8%; Score 44; DB 2; Length 329;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNVT 13
    :|||: |||: |||:
Db 91 KNPVTHFNSIVS 103

RESULT 13
T46577
arylsulfatase (EC 3.1.6.1) [validated] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: T46577
R;Baker, D.L.; Paletta, J.V.
submitted to the EMBL Data Library, February 1997
A;Description: Molecular characterization of the arylsulfatase gene of Neurospora crassa
A;Reference number: 223090
A;Accession: T46577
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-639 <BAK>
A;Cross-references: UNIPROT:O43113; UNIPARC:UPI000006B2E2; EMBL:U89492; PIDN:AAC02716.1
A;Experimental source: strain wild type 74-OR23-1A
C;Genetics:
A;Gene: ars-1
A;Map position: 7
A;Introns: 115/1; 518/3
C;Function:
A;Description: EC 3.1.6.1 [validated, MUID:89384589]
A;Note: Genes are expressed under conditions of sulfur limitation and are under coordina
C;Superfamily: arylsulfatase, plant type
C;Keywords: sulfuric ester hydrolase

Query Match      46.8%; Score 44; DB 2; Length 639;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 HFFKNIVTPRTP 17
    |||: |||: |||:
Db 282 HLFDPDIVPRT 293

RESULT 14
S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
```

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C;Species: Pisaster ochraceus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S12904
R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A;Title: Identification of the sites in myelin basic protein that are phosphorylated by
A;Reference number: S12904; MUID:91032186; PMID:1699809
A;Accession: S12904
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <SAN>
A;Cross-references: UNIPROT:Q7M3M4; UNIPARC:UPI000017BF0C
C;Keywords: phosphotransferase

Query Match      45.7%; Score 43; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NIVTPRTP 17
    ||||| |||
Db 1 NIVTPRTP 8

RESULT 15
C89965
conserved hypothetical protein SA1613 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89965
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hizamatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <KUR>
A;Cross-references: UNIPROT:Q99T75; UNIPARC:UPI000013B193; GB:BA000018; PID:gl3701588;
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1613
C;Superfamily: conserved hypothetical protein HI1000

Query Match      45.7%; Score 43; DB 2; Length 85;
Best Local Similarity 35.7%; Pred. No. 3.3;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 VVHFFKNIVTPRTP 17
    :|||: |||: |||:
Db 8 MHFYQRFISPLTP 21

Search completed: February 22, 2006, 21:38:18
Job time : 2.7323 secs
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:11 ; Search time 11.1572 Seconds
(without alignments)
669.475 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	3 AAY69395	Peptide d
2	94	100.0	17	5 AAO20308	Myelin ba
3	94	100.0	17	5 AAE26359	Peptide r
4	94	100.0	17	5 AAE23935	Peptide a
5	94	100.0	17	6 ABP97941	Amino aci
6	94	100.0	17	6 ABR5063	Glycopept
7	94	100.0	17	6 AAO19672	Human mye
8	94	100.0	17	7 ADE50773	Wild-type
9	94	100.0	17	7 ADW36476	HLA bindi
10	94	100.0	17	7 ADW35045	HLA bindi
11	94	100.0	17	7 ADW33812	HLA bindi
12	94	100.0	17	8 ADK67704	Human mye
13	94	100.0	17	8 ADL18291	Human mye
14	94	100.0	17	9 AEB77584	MBP pepti
15	94	100.0	17	9 AEB86495	Myelin ba
16	94	100.0	18	2 AAR44115	Human mye
17	94	100.0	18	2 AAR95357	Residues
18	94	100.0	18	2 AAW73600	Human mye
19	94	100.0	18	3 AAY66533	Myelin ba
20	94	100.0	19	2 AAR32295	Sequence
21	94	100.0	19	2 AAR44114	Human mye
22	94	100.0	19	2 AAR44123	Human mye
23	94	100.0	19	2 AAR85132	Human MBP
24	94	100.0	19	2 AAW05719	Residues

25	94	100.0	19	2 AAR95366	Residues
26	94	100.0	19	2 AAR95355	Residues
27	94	100.0	19	2 AAR95358	Residues
28	94	100.0	19	2 AAW34183	Bt-MBP (84
29	94	100.0	19	2 AAW34180	Residues
30	94	100.0	19	2 AAW18021	Human BPP
31	94	100.0	19	2 AAW44071	Human mye
32	94	100.0	19	2 AAW73607	Human mye
33	94	100.0	19	2 AAW73616	Human mye
34	94	100.0	19	3 AAY58992	Myelin ba
35	94	100.0	19	3 AAY85560	Human MBP
36	94	100.0	19	3 AAY85550	Human MBP
37	94	100.0	19	3 AAY66532	Myelin ba
38	94	100.0	19	3 AAY66543	Myelin ba
39	94	100.0	19	3 AAB12618	Human mye
40	94	100.0	19	3 AAB12613	Human mye
41	94	100.0	19	4 AAM99040	Vaccine r
42	94	100.0	19	4 AAB74440	Ovalbumin
43	94	100.0	19	4 AAG65171	Myelin ba
44	94	100.0	19	5 ABG31665	Myelin ba
45	94	100.0	19	7 ADW35009	HLA bindi

ALIGNMENTS

RESULT 1
AAY69395
ID AAY69395 standard; peptide; 17 AA.
XX
AC AAY69395;
XX
DT 19-JUN-2000 (first entry)
XX
DE Peptide derived from a human myelin basic protein.
XX
KW Human; myelin basic protein; oligodendroglial cell; Th2 immune response;
KW Th2-type cytokine; analogue; multiple sclerosis.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO200011027-A1.
XX
PD 02-MAR-2000.
XX
PF 19-AUG-1999; 99WO-US019033.
XX
PR 20-AUG-1998; 98US-00137759.
XX
(NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
PI Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;
DR WPI; 2000-224661/19.
PT Inducing a Th2 immune response and a persistent systemic immune response
PT to myelin basic protein, MBP, or a peptide analog of MBP for use in
PT treating multiple sclerosis, by administering compositions comprising
XX peptide analogs of MBP.
XX Example 10; Fig 8; 112pp; English.
XX
CC The present sequence represents a peptide derived from human myelin basic
CC protein. Myelin basic protein is found in the cytoplasm of human
CC oligodendroglial cells. Peptide analogue derived from the present
CC sequence is administered to a patient in need to induce a Th2 immune
CC response (i.e. production of T cells producing one or more Th2-type
CC cytokines) and/or a persistent systemic immune response to myelin basic
CC protein. These peptide analogues are at least seven amino acids long,
CC derived from residues 83-99 of human myelin basic protein and altered

CC from the native sequence at least at positions 91, 95 or 97. The peptide
 CC analogs are especially useful in the treatment of multiple sclerosis
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTPRTP 17
 |||||
 RESULT 2
 AAO20308
 ID AAO20308 standard; peptide; 17 AA.
 XX
 AC AAO20308;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Myelin basic protein (MBP) epitope peptide region 83-99.
 XX
 KW MBP, myelin basic protein; epitope; antiaesthatic; tolerogenic peptide;
 KW dermatological; antiallergic; neuroprotective; antithyroid; antinaemic;
 KW vasotropic; antiinflammatory; immunosuppressive; antidiabetic; class I;
 KW major histocompatibility complex; MHC; class II; autoimmune thyroiditis;
 KW hypersensitivity disorder; antigen; allergy; extrinsic asthma; utricaria;
 KW autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis;
 KW autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis;
 KW systemic sclerosis; polymyositis; diabetes; transplant rejection;
 KW antiviral CD8+.
 XX
 OS Unidentified.
 XX
 PN WO200216410-A2.
 XX
 XX 28-FEB-2002.
 PD
 XX
 PF 17-AUG-2001; 2001WO-GB003702.
 XX
 XX 21-AUG-2000; 2000GB-00020618.
 PR
 PR 14-JUN-2001; 2001GB-00014547.
 XX
 XX (UYBR-) UNIV BRISTOL.
 PA
 XX
 PI Wraith DC, Anderton SM, Mazza G, Ponsford M, Streeter HB;
 XX
 XX WPT; 2002-292056/33.
 DR
 XX
 PT Selecting tolerogenic peptide useful for treating autoimmune diseases
 PT e.g. multiple sclerosis, involves selecting peptide which binds major
 PT histocompatibility complex class I or II molecule without further
 PT processing.
 PT
 XX
 PS Claim 12; Page 28; 55pp; English.
 XX
 CC The invention relates to a method for selecting a tolerogenic peptide,
 CC comprising selecting a peptide which is capable of binding to a major
 CC histocompatibility complex (MHC) class I or II molecule without further
 CC processing. The peptides of the invention are useful for preventing a
 CC disease such as hypersensitivity disorder, and also for treating and/or
 CC preventing a disease in a subject. The method involves identifying an
 CC antigen for the disease, identifying an epitope (antigen processing
 CC independent epitope) for the antigen, and administering the epitope to
 CC the subject. The peptides of the invention are also useful for treating
 CC allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis,
 CC utricaria, autoimmune diseases such as multiple sclerosis, autoimmune
 CC thyroiditis, Grave's disease, systemic sclerosis, sarcoidosis, autoimmune
 CC haemolytic anaemia, polymyositis, diabetes, etc, and transplant
 CC rejection. The peptides are also useful for modifying antiviral CD8+
 CC responses in a tolerogenic fashion. This sequence represents an epitope

CC of the invention of peptide region 83-99 of Myelin basic protein (MBP)
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTPRTP 17
 |||||
 RESULT 3
 AAE26359
 ID AAE26359 standard; peptide; 17 AA.
 XX
 AC AAE26359;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Peptide related to myelin basic protein.
 XX
 KW Th2 immune response; myelin basic protein; MBP; vaccine; MS;
 KW multiple sclerosis; antisclerotic.
 XX
 OS Unidentified.
 XX
 PN US6379670-B1.
 XX
 PD 30-APR-2002.
 XX
 PF 19-AUG-1999; 99US-00378244.
 XX
 PR 18-NOV-1994; 94US-00342408.
 PR 20-AUG-1998; 98US-00137759.
 XX
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PA (NOVS) NOVARTIS AG.
 XX
 PI Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;
 XX
 XX WPI; 2002-461895/49.
 DR
 XX
 PT Inducing Th2 immune responses to Myelin Basic Protein (MBP) by
 PT administering the MBP peptide analog CGP 77116, useful for treating
 PT Multiple Sclerosis.
 PT
 XX
 PS Disclosure; Col 35-36; 49pp; English.
 XX
 CC The present invention relates to a novel method for inducing Th2 immune
 CC responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a
 CC patient. The method involves administering a composition comprising the
 CC MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for
 CC treating multiple sclerosis (MS). Sequences of the invention are also
 CC used as vaccines. The present sequence is a peptide related to human MBP
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTPRTP 17
 |||||
 RESULT 4
 AAE23935
 ID AAE23935 standard; peptide; 17 AA.
 XX
 AC AAE23935;

XX 10-SEP-2002 (first entry)
 XX Peptide analogue used in the invention.
 XX Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;
 KW immunosuppressive; T-cell receptor; therapy.
 XX Unidentified.
 OS WO200216434-A1.
 XX PN 28-FEB-2002.
 XX PD 22-AUG-2000; 2000WO-US022988.
 XX PF 22-AUG-2000; 2000WO-US022988.
 XX PR (BAYU) BAYLOR COLLEGE MEDICINE.
 XX PA Zhang JZ;
 XX PI WPI; 2002-454317/48.
 XX DR A novel peptide used in the treatment of autoimmune disease e.g. multiple
 XX PT sclerosis.
 XX PS Example 2; Fig 2; 64pp; English.
 XX PS The invention relates to a peptide used in the treatment of autoimmune
 CC disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-
 CC cell receptor sequence found in some MS patients and methods for its
 CC detection. T cell receptors comprise alpha and beta chains, with beta
 CC chains comprising the following regions from N-terminus to C-terminus:
 CC Vbeta-alpha-Jbeta-Cbeta. T cell receptors naturally vary in the Vbeta-
 CC Dbeta-alpha region. The peptides of the invention are used for treating
 CC autoimmune disease e.g. multiple sclerosis. The present sequence is a
 CC peptide analogue used in the exemplification of the invention
 XX SQ Sequence 17 AA;
 XX Query Match 100.0%; Score 94; DB 5; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 7e-09;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 ENPVVHFFKNIPTPT 17
 XX DB 1 ENPVVHFFKNIPTPT 17
 XX RESULT 5
 XX ID ABP97941 standard; peptide; 17 AA.
 XX AC ABP97941;
 XX DT 17-JUN-2003 (first entry)
 XX DE Amino acid sequence of a glycopeptide.
 XX KW Glycopeptide; serum; immunoabsorption column; antibody;
 KW multiple sclerosis.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "H attached"
 FT Modified-site 2 /note= "glycosylated residue"
 FT Modified-site 17 /note= "OH attached"
 XX

PN WO2003009887-A2.
 XX 06-FEB-2003.
 XX 25-JUL-2002; 2002WO-EP008274.
 XX 25-JUL-2001; 2001IT-FI000144.
 XX (UYFI-) UNIV FIRENZE.
 XX Pinto F, Papini AM, Chelli M, Rovero P, Lolli F;
 XX WPI; 2003-312632/30.
 XX Immunoabsorption column, useful for treating multiple sclerosis, contains
 PT glycopeptides able to react with disease-specific autoantibodies.
 XX Claim 4; Page 6; 13pp; English.
 XX ABP97937-44 represent glycopeptides of a formula given in the
 CC specification. The glycopeptides are used to produce columns of the
 CC invention. The specification describes immunoabsorption columns,
 CC containing conjugates comprising glycopeptides which are able to
 CC recognize antibodies implicated in multiple sclerosis. The column removes
 CC harmful antibodies selectively, leaving all other components of the serum
 CC unchanged. The column is used to treat multiple sclerosis
 XX SQ Sequence 17 AA;
 XX Query Match 100.0%; Score 94; DB 6; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 7e-09;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 ENPVVHFFKNIPTPT 17
 XX DB 1 ENPVVHFFKNIPTPT 17
 XX RESULT 6
 XX ID ABR56063 standard; peptide; 17 AA.
 XX AC ABR56063;
 XX DT 06-AUG-2003 (first entry)
 XX DE Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.
 XX KW Glycopeptide; neuroprotective; autoantibody; multiple sclerosis.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 2 /note= "Asn(Glc)"
 XX WO2003000733-A2.
 XX 03-JAN-2003.
 XX 19-JUN-2002; 2002WO-EP006767.
 XX 22-JUN-2001; 2001IT-FI000114.
 XX (UYFI-) UNIV FIRENZE.
 XX Papini AM, Chelli M, Rovero P, Lolli F;
 XX WPI; 2003-354383/33.
 XX Novel glycopeptides comprising a specific tetrapeptide, useful as
 FT diagnostic tools for identifying multiple sclerosis.
 XX

PS Claim 7; Page 12; 14pp; English.

XX The present invention relates to glycopeptides (ABR56059-ABR56066). The glycopeptides have high specificity in recognizing autoantibodies involved in multiple sclerosis pathology, and thus are effectively used in diagnosis and treatment for multiple sclerosis

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | |
Db 1 ENPVVHFFKNIIVTRTP 17

RESULT 7

AAO19672

ID AAO19672 standard; peptide; 17 AA.

XX

AC AAO19672;

XX

DT 28-MAR-2003 (first entry)

XX

DE Human myelin basic protein MBP minimal epitope.

XX

Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP; Fc epsilon receptor; autoimmune disease; constant region; heavy chain; antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2; antiarthritic; antirheumatic; antidiabetic; neuroprotective; myelin basic protein; minimal epitope.

XX

Homo sapiens.

OS

XX

PN WO200298317-A2.

XX

XX

PD 07-NOV-2002.

XX

PF 01-MAY-2002; 2002WO-US013527.

XX

PR 01-MAY-2001; 2001US-00847208.

PR 24-OCT-2001; 2001US-00000439.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Saxon A, Zhang K, Zhu D;

XX

WPI; 2003-103456/09.

DR

XX

PT New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

PT

PS Claim 23; Page 116; 116pp; English.

XX

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (Fc epsilon R). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-1 diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human myelin

CC

CC basic protein minimal epitope which can be used in a fusion protein of the invention

CC

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | |
Db 1 ENPVVHFFKNIIVTRTP 17

RESULT 8

ADE50773

ID ADE50773 standard; peptide; 17 AA.

XX

AC ADE50773;

XX

DT 29-JAN-2004 (first entry)

XX

DE Wild-type human myelin basic protein peptide analog.

XX

Human; Th2; immune response; myelin basic protein; peptide analog; proteolysis; multiple sclerosis; neuroprotective; gene therapy.

KW

XX

OS Homo sapiens.

XX

US2002176866-A1.

XX

PD 28-NOV-2002.

XX

PF 20-MAR-2002; 2002US-00104973.

XX

PR 18-NOV-1994; 94US-00342408.

PR 20-AUG-1998; 98US-00137759.

PR 19-AUG-1999; 99US-00378244.

XX

PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX

Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;

XX

WPI; 2003-615722/58.

DR

XX

PT Inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, useful for treating multiple sclerosis, comprises administering an amount of a pharmaceutical composition comprising a peptide analog.

PT

PS Disclosure; SEQ ID NO 3; 52pp; English.

XX

The invention discloses a method for inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, comprising administering a composition comprising a peptide analog in combination with a carrier/adjuvant or diluent. The peptide analog comprises at least 7 amino acids selected from residues 83 to 99 of human myelin basic protein, where: the L-lysine at position 91, L-arginine at position 97 or L-threonine at position 95, is altered to another amino acid, and one to three L-amino acids selected from valine at position 86 or 87, histidine at position 88, threonine at position 95 or 98, and proline at position 99 are altered to an amino acid other than the amino acid present in the native protein at that position or the L-lysine at position 91 is altered to another amino acid and the N- and/or C-terminal amino acid are altered to another amino acid, such that upon administration of the peptide analog in vivo proteolysis is reduced. The peptide analog comprises 7-17 amino acids and one to four additional altered residues. The N-terminal amino acid is residue 83 of human myelin basic protein. At least one of the additional L-amino acids selected from residues 83 to 90 and 92 to 99 is substituted with a charged amino acid. The method is useful for treating multiple sclerosis using peptide analogs of human myelin basic protein. The sequence presented is the wild-type human myelin basic protein peptide analog.

CC

XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 1 ENPVVHFFKNIIVTRTP 17
 |||||

RESULT 9
 ADW36476
 ID ADW36476 standard; peptide; 17 AA.
 XX
 AC ADW36476;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #7226.
 XX
 KW Viricide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003040165-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 1 ENPVVHFFKNIIVTRTP 17
 |||||

RESULT 11
 ADW33812

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 1 ENPVVHFFKNIIVTRTP 17
 |||||

RESULT 10
 ADW35045
 ID ADW35045 standard; peptide; 17 AA.
 XX
 AC ADW35045;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #5795.
 XX
 KW Viricide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003040165-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 1 ENPVVHFFKNIIVTRTP 17
 |||||

RESULT 11
 ADW33812

ID ADW33812 standard; peptide; 17 AA.
 AC ADW33812;
 XX
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #4562.
 XX
 KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.
 XX
 XX Unidentified.
 OS
 XX WO2003040165-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 18-OCT-2001; 2001WO-US051650.
 PP
 XX 19-OCT-2000; 2000US-0242350P.
 PR
 XX 20-APR-2001; 2001US-0285624P.
 PR
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S;
 PI
 XX WPI; 2003-441519/41.
 DR
 XX
 XX New composition comprising at least one peptide having allele-specific
 XX binding motifs for HLA, useful for preventing, treating or diagnosing
 XX viral diseases and cancer.
 PT
 PT
 PT
 XX Claim 1; Page 52-379; 382pp; English.
 PS
 XX
 XX The invention relates to a composition comprising at least one peptide
 XX having an isolated, prepared epitope selected from any of the sequences
 XX from 30 lists given in the specification. Also disclosed is a method for
 XX inducing a cytotoxic T cell response against a pre-selected antigen in a
 XX patient expressing a specific MHC class I allele by contacting cytotoxic
 XX T cells from the patient with the composition cited above. The
 XX composition comprises an epitope that is joined by an amino acid linker.
 XX The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 XX bound to an HLA molecule on the antigen-presenting cell, where when an A2
 XX -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 XX binds to a complex of the HLA molecule and the epitope. Specifically
 XX claimed are peptides having allele-specific binding motifs for HLA. The
 XX compositions and methods are useful for preventing, treating or
 XX diagnosing viral diseases and cancer. The peptide epitopes are useful as
 XX diagnostic agents for evaluating immune responses, for making antibodies
 XX and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 XX ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIVTPRTP 17
 DB 1 ENPVVHFFKNIVTPRTP 17
 RESULT 12
 ADK67704
 ID ADK67704 standard; peptide; 17 AA.
 XX
 AC ADK67704;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Human myelin basic protein peptide fragment MBP-1 (aa110-126).
 DE

XX
 KW Human; myelin basic protein; vaccine; multiple sclerosis; T cell.
 XX
 OS Homo sapiens.
 XX
 XX WO2004015070-A2.
 PN
 XX 19-FEB-2004.
 PD
 XX 06-AUG-2003; 2003WO-US024548.
 PF
 XX 08-AUG-2002; 2002US-0402521P.
 PR
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (OPEX-) OPEXA PHARM INC.
 PA
 XX Zhang JZ;
 PI
 XX WPI; 2004-180654/17.
 DR
 XX Isolating one or more T cells specific for an antigen of interest
 XX comprises incubating a T cell sample with an antigen, useful for
 XX diagnosing or treating multiple sclerosis, psoriasis, thyroiditis,
 XX diabetes and rheumatoid arthritis.
 XX
 XX Example 1; SEQ ID NO 1; 38pp; English.
 PS
 XX
 XX The present invention is direct to methods of isolating antigen specific
 XX T cells, especially T cells specific for self or autoantigens. This
 XX comprises incubating a sample of T cells obtained from a patient with the
 XX antigen and selecting T cells that express one or more of first markers
 XX selected from CD69, CD4, CD25, CD36 and HLA-DR, and one or more second
 XX markers selected from interleukin-2, interferon-gamma, tumour necrosis
 XX factor alpha, interleukin-5, interleukin-10 and interleukin-12. The
 XX methods are useful for isolating autoreactive T cells which play a role
 XX in the pathogenesis of autoimmune diseases. The methods also permit the
 XX diagnosis of autoimmune disease as well as monitoring the progression of
 XX the disease and for monitoring the efficacy of treatment. The methods
 XX allow the preparation of autologous T cell vaccines for the treatment of
 XX T cell related autoimmune diseases. Vaccine preparation involves the
 XX isolation of antigen-specific T cells optionally followed by culturing
 XX steps which allow the expansion of the population of isolated antigen-
 XX specific T cells. An example from the invention describes the isolation
 XX of myelin-reactive T cells for T cell vaccination. Peripheral blood
 XX mononuclear cells were isolated from the blood of multiple sclerosis
 XX patients and incubated with peptides comprising known immunodominant
 XX regions of 3 myelin proteins. These included the present peptide, which
 XX comprises amino acids 110-126 of human myelin basic protein. Cells were
 XX then selected for the expression of gene products indicative of activated
 XX T cells, and myelin-reactive T cells were propagated in culture. The
 XX methods and compositions of the invention are useful for the diagnosis
 XX and/or treatment of autoimmune diseases or T cell associated conditions
 XX such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus
 XX erythematosus, autoimmune thyroiditis, Grave's disease, inflammatory
 XX bowel disease, diabetes and rheumatoid arthritis.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIVTPRTP 17
 DB 1 ENPVVHFFKNIVTPRTP 17
 RESULT 13
 ADL18291
 ID ADL18291 standard; peptide; 17 AA.
 XX
 AC ADL18291;
 XX

DT 20-MAY-2004 (first entry)
 XX Human myelin basic protein (MBP), peptide #2.
 DE
 XX
 XX Demyelinating disease; neuron-specific antigen; human;
 KW myelin basic protein; MBP; myelin oligodendrocyte glycoprotein;
 KW myelin associated glycoprotein; MAG; proteolipid protein; PLP;
 KW small heat shock protein; transaldolase; Glial fibrillary protein;
 KW S-100 protein; cross-reactive peptide; glutamate receptor;
 KW phosphodiesterase; multiple sclerosis.
 XX
 XX Homo sapiens.
 OS
 XX US2004043431-A1.
 PN
 XX
 XX 04-MAR-2004.
 PD
 XX
 XX 29-AUG-2002; 2002US-00233892.
 PF
 XX
 XX 29-AUG-2002; 2002US-00233892.
 PR
 XX
 XX (VOJD/) VOJDANI A.
 PA
 XX
 XX Vojdani A;
 PI
 XX
 XX WPI; 2004-313756/29.
 DR
 XX
 XX Diagnosing likelihood and severity of demyelinating disease, by
 PT determining antibodies against neuron-specific antigen, comparing level
 PT of detected antibodies with normal level for detecting absence/likelihood
 PT of demyelinating disease.
 XX
 XX Claim 6; SEQ ID NO 2; 27pp; English.
 PS
 XX
 XX The present invention relates to a method of diagnosing the likelihood
 CC and severity of demyelinating diseases. The method involves determining
 CC antibodies against neuron-specific antigen in sample, comparing the level
 CC of antibodies with the normal level of antibodies, where normal level of
 CC antibodies for neuron-specific antigen indicates optimal conditions, lower
 CC than or higher than normal level of antibodies for the antigen indicate
 CC an absence of or a likelihood of demyelinating diseases, respectively.
 CC The neuron-specific antigen is chosen from myelin basic protein (MBP),
 CC myelin oligodendrocyte glycoprotein, myelin associated glycoprotein
 CC (MAG), proteolipid protein (PLP), small heat shock protein,
 CC transaldolase, Glial fibrillary protein, S-100 protein, cross-reactive
 CC peptide from dietary protein, cross-reactive peptide from infectious
 CC agent, glutamate receptor, and phosphodiesterase. The immunoassay is an
 CC enzyme linked immunosorbent assay (ELISA) test. The method is useful for
 CC diagnosing the likelihood and severity of demyelinating diseases such as
 CC multiple sclerosis in a patient. The present sequence represents a
 CC peptide from human MBP.
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 94; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIIVTRTP 17
 Db 1 ENPVVHFFKNIIVTRTP 17
 RESULT 14
 AEB77584
 ID AEB77584 standard; peptide; 17 AA.
 XX
 XX AEB77584;
 AC
 XX 06-OCT-2005 (first entry)
 DT
 XX MBP peptide - SEQ ID 6.
 DE
 XX

KW autism; nootropic; asperger syndrome; MBP.
 XX Unidentified.
 OS
 XX US2005170333-A1.
 PN
 XX 04-AUG-2005.
 PD
 XX
 XX 03-FEB-2004; 2004US-00770712.
 PF
 XX
 XX 03-FEB-2004; 2004US-00770712.
 PR
 XX
 XX (VOJD/) VOJDANI A.
 PA
 XX
 XX Vojdani A;
 PI
 XX
 XX WPI; 2005-562713/57.
 DR
 XX
 XX Determining etiology of autistic spectrum disorder in patient, by
 PT determining level of infectious agent/toxic chemical/dietary protein
 PT derived antigen in samples of patient, comparing it with normal level of
 PT antigens of control subjects.
 XX
 XX Disclosure; SEQ ID NO 6; 89pp; English.
 PS
 XX
 XX The invention comprises a method of determining etiology of an autistic
 CC spectrum disorder in a patient. The method involves determining the level
 CC of an infectious agent, toxic chemical, or dietary protein derived
 CC antigen, or their antibodies in samples of patient, and comparing
 CC antigens/antibodies levels with normal levels of antigens/antibodies from
 CC control subjects. The method of the invention is useful for determining
 CC the etiology of an autistic spectrum disorder, such as autism, pervasive
 CC development disorder and Asperger's syndrome. The present amino acid
 CC sequence represents a peptide that was used in the exemplification of the
 CC invention.
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 94; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIIVTRTP 17
 Db 1 ENPVVHFFKNIIVTRTP 17
 RESULT 15
 AEB86495
 ID AEB86495 standard; peptide; 17 AA.
 XX
 XX AEB86495;
 AC
 XX 20-OCT-2005 (first entry)
 DT
 XX
 XX Myelin basic protein (MBP) peptide, amino acids 83-99.
 DE
 XX
 XX pharmaceutical; t-lymphocyte; antigen; multiple sclerosis;
 KW autoimmune disease; immune disorder; immune stimulation; immunity;
 KW autoimmunity; immunosuppressive; neuroprotective; antiarthritic;
 KW antirheumatic; antiinflammatory; myelin; myelin basic protein; MBP.
 XX
 XX Unidentified.
 OS
 XX WO2005074579-A2.
 PN
 XX
 XX 18-AUG-2005.
 PD
 XX
 XX 02-FEB-2005; 2005WO-US002962.
 PF
 XX
 XX 02-FEB-2004; 2004US-0541397P.
 PR
 XX
 XX (MIXT-) MIXTURE SCI INC.
 PA

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Houghten RA, Pinilla C, Martin R, Sturzebecher C;
 PI Shukaliak-Quandt J, McFarland HF;
 XX
 DR WPI; 2005-555771/56.
 XX
 FT Complex peptide mixture having immunomodulatory effects, useful for
 FT preparing medicament for treating autoimmune disease e.g. multiple
 FT sclerosis, rheumatoid arthritis, for preparing medicament for stimulating
 FT immune cell.
 XX
 PS Example; Page 22; 51pp; English.
 XX
 CC The invention relates to complex peptide mixtures comprises several
 CC peptides having 8-20 amino acids, where the mixture comprises peptides
 CC having a degree of diversity at defined positions in the peptide chain,
 CC where the degree of diversity in the defined position is different from
 CC other defined positions, and where in the majority of the mixture, the
 CC peptides includes Ala, Glu, Lys and Tyr and no other amino acids, in at
 CC least four positions. Also described are: (1) a method of creating a high
 CC affinity peptide ligand of a defined formula for a receptor of a T cell
 CC that is reactive to a myelin antigen, copolymer, or an active mixture;
 CC and (2) a method of enhancing a biological property of a complex mixture
 CC of peptides, peptidomimetics or peptides and peptidomimetics. The
 CC complex peptide mixture is useful in the preparation of a medicament for
 CC treating a disease such as multiple sclerosis (MS) and experimental
 CC autoimmune encephalomyelitis (EAE). It is also useful for preparing a
 CC medicament for stimulating an immune cell, or for suppression of an
 CC immune reaction (e.g. autoimmune reaction) to an antigen derived from
 CC myelin. This sequence represents a myelin peptide used in the examples of
 CC the present invention.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTRTP 17

Search completed: February 22, 2006, 21:30:49
 Job time : 14.1572 secs

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:24 ; Search time 154.266 Seconds
(without alignments)
1061.041 Million cell updates/sec

Title: US-10-000-439-3
Perfect score: 1260
Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNYQRRSLSPGK 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 IGHG1_HUMAN	P01857 homo sapien
2	1225	97.2	465	2 Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	1225	97.2	466	2 Q6IN78_HUMAN	Q6in78 homo sapien
4	1225	97.2	469	2 Q569F4_HUMAN	Q569f4 homo sapien
5	1225	97.2	469	2 Q7Z7P5_HUMAN	Q7z7p5 homo sapien
6	1225	97.2	470	2 Q7Z5W1_HUMAN	Q7z5w1 homo sapien
7	1225	97.2	470	2 Q6FJA4_HUMAN	Q6fja4 homo sapien
8	1225	97.2	472	2 Q6N089_HUMAN	Q6n089 homo sapien
9	1225	97.2	475	2 Q5EFES_HUMAN	Q5efes homo sapien
10	1225	97.2	475	2 Q6GMW7_HUMAN	Q6gmw7 homo sapien
11	1225	97.2	476	2 Q6GNX1_HUMAN	Q6gmx1 homo sapien
12	1225	97.2	679	2 Q96PQ8_HUMAN	Q96pq8 homo sapien
13	1221	96.9	473	2 Q6P055_HUMAN	Q6p055 homo sapien
14	1221	96.9	475	2 Q6MZQ6_HUMAN	Q6mzq6 homo sapien
15	1221	96.9	480	2 Q6N094_HUMAN	Q6n094 homo sapien
16	1221	96.9	481	2 Q6N097_HUMAN	Q6n097 homo sapien
17	1221	96.9	482	2 Q7Z351_HUMAN	Q7z351 homo sapien
18	1219	96.7	348	2 Q6PYX1_HUMAN	Q6pyx1 homo sapien
19	1219	96.7	473	2 Q6MZV7_HUMAN	Q6mzv7 homo sapien
20	1219	96.7	478	2 Q6PI81_HUMAN	Q6pi81 homo sapien
21	1219	96.7	480	2 Q6PJF1_HUMAN	Q6pjf1 homo sapien
22	1218	96.7	466	2 Q6N096_HUMAN	Q6n096 homo sapien
23	1214	96.3	475	2 Q6N095_HUMAN	Q6n095 homo sapien
24	1214	96.3	544	2 Q6FJ95_HUMAN	Q6fj95 homo sapien
25	1196	94.9	487	2 Q6SZL2_HUMAN	Q6szl2 homo sapien
26	1164	92.4	475	2 Q5RE17_HUMAN	Q5re17 pongo pygma
27	1138	90.3	354	2 Q86TF2_HUMAN	Q86tf2 homo sapien
28	1138	90.3	518	2 Q6N030_HUMAN	Q6n030 homo sapien
29	1138	90.3	519	2 Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	1134	90.0	521	2 Q8N4Y9_HUMAN	Q8n4y9 homo sapien
31	1128	89.5	290	1 IGHG3_HUMAN	P01860 homo sapien

RESULT 1	IGHG1_HUMAN	STANDARD;	PRT;	330 AA.
ID	IGHG1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	PROTEIN SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal			
RT	IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic			
RT	peptides of the H-chain, alignment of the tryptic peptides and			
RT	discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			

Q8NF17 homo sapien
P01859 homo sapien
Q6N093 homo sapien
Q6MZU6 homo sapien
Q6P6C4 homo sapien
P01861 homo sapien
Q8TC63 homo sapien
Q68CN4 homo sapien
Q6MX77 homo sapien
P01870 oryctolagus
Q95M34 equus caball
P01862 cavia porce
P20761 rattus norv
Q5M839 rattus norv

RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
RN [9]
RP MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC G1M(3) markers, 239-D and 241-L. KOL and EU sequences have the
CC G1M(1) marker and the G1M (non-1) markers.
CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
DR PIR; A93433; GHU.
DR PDB; 1A77; X-ray; H=1-103.
DR PDB; 1AOK; X-ray; H=1-103.
DR PDB; 1DSB; X-ray; B/H=1-101.
DR PDB; 1DS1; X-ray; H=1-101.
DR PDB; 1DV6; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1H2H; X-ray; H/K=1-330.
DR PDB; 1I17; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1LOQ; X-ray; A/B=119-330.
DR PDB; 1TB3; X-ray; A/B=107-330.
DR PDB; 2RCS; X-ray; H=1-103.
DR HGNC; HGNC:5525; IGHG1.
DR MTM; 147100; --
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
FT REGION 1 98
CHI.

FT	REGION	99	110	Hinge.
FT	REGION	111	223	CH2.
FT	REGION	224	330	CH3.
FT	CARBOHYD	180	180	N-linked (GlcNAc. . .).
FT	DISULFID	27	83	
FT	DISULFID	103	103	Interchain (with light chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	VARIANT	97	97	
FT	VARIANT	239	239	K -> R (in G1M(3) marker).
FT	VARIANT	241	241	/FTID=VAR_003886.
FT	VARIANT	241	241	D -> E (in G1M(non-1) marker).
FT	VARIANT	241	241	/FTID=VAR_003887.
FT	VARIANT	241	241	L -> M (in G1M(non-1) marker).
FT	VARIANT	241	241	/FTID=VAR_003888.
FT	NON_TER	1	1	
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	TURN	176	177	
FT	STRAND	179	180	
FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 97.2%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 5.9e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 99 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKT 120
Db 159 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQGPENNYKTTTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQGPENNYKTTTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 232
Db 279 PVLDSGSGFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
Q6GMX6 HUMAN
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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Query Match 97.2%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 9, 1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 234 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293
Qy 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKT 120
Db 234 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 353
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQGPENNYKTTTP 180
Db 354 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQGPENNYKTTTP 413
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 232
Db 414 PVLDSGSGFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 465

RESULT 3
Q6IN78 HUMAN
ID Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
```


DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8DSBE12BAAF795C CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 469;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 238 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297
QY 61 NNYVDGVEVHNKTKPRREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 298 NNYVDGVEVHNKTKPRREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 357
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 358 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 417
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 418 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 469

RESULT 6
Q725W1 HUMAN
ID Q725W1_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -, mRNA.
DR HSP; P01857; IZH.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003597; IG_c1.

DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 61 NNYVDGVEVHNKTKPRREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 299 NNYVDGVEVHNKTKPRREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 359 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 418
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 419 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 7
Q6PJA4 HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSP; P01861; IADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 470 AA; 51716 MW; 7849556A11FD7D99 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKKVSNNKALPAPIEKT 120
DB 299 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKKVSNNKALPAPIEKT 358
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 418
QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
DB 419 PVLDSGGSFLLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 8
Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
ID Q6N089_HUMAN
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA FoBo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -; mRNA.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKKVSNNKALPAPIEKT 120
DB 299 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKKVSNNKALPAPIEKT 358
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 418
QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
DB 419 PVLDSGGSFLLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 9
Q5EFES HUMAN PRELIMINARY; PRT; 475 AA.
ID Q5EFES_HUMAN
AC Q5EFES;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC "Sequence determination of the recombinant human anti-Rhd monoclonal antibody T125.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY849492; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW SIGNAL.
FT CHAIN 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400CD7D2859 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKKVSNNKALPAPIEKT 120
DB 304 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKKVSNNKALPAPIEKT 363
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
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Db 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLIVKGFPSPDIWESNGQENNYKTTTP 423
181 PVLDSVGSFFLYSKLTVDSKRWQGNVFSQVWHEALHNHYQOORSLSLSPGK 232
424 PVLDSGDSFFLYSKLTVDSKRWQGNVFSQVWHEALHNHYQOORSLSLSPGK 475

RESULT 10
Q6GMW7 HUMAN
ID Q6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2AIPES5D736860F8 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCTCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
244 EPKSCDKTHCTCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 303
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Qy 61 NWYVDGVVHNVTKPRBEQYNSTYRVVSVLTVLHQNWNGKYEYCKVSNKALPAPIEKT 120
304 NWYVDGVVHNVTKPRBEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKT 363
121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLIVKGFPSPDIWESNGQENNYKTTTP 180
364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLIVKGFPSPDIWESNGQENNYKTTTP 423

181 PVLDSVGSFFLYSKLTVDSKRWQGNVFSQVWHEALHNHYQOORSLSLSPGK 232
424 PVLDSGDSFFLYSKLTVDSKRWQGNVFSQVWHEALHNHYQOORSLSLSPGK 475

RESULT 11
Q6GMX1 HUMAN
ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
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Query Match

97.2%; Score 1225; DB 2; Length 476;

Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 245 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 304

QY 61 NWYDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120
DB 305 NWYDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 364

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 424

QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 425 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 476

RESULT 12
Q96PQ8_HUMAN
ID Q96PQ8_HUMAN PRELIMINARY; PRT; 679 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RL calls for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Hu Z., Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272774; AAK58686.2; -, mRNA.
DR HSP; P08709; IKLI.
DR SMR; Q96PQ8; 39-180, 191-444, 447-679.
DR Ensembl; ENSG00000057593; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gfa; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00020; TYPD_SPG; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00835; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 679;
Best Local Similarity 97.0%; Pred. No. 1.5e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 448 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 507

QY 61 NWYDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120
DB 508 NWYDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 567

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 568 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 627

QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 628 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 679

RESULT 13
Q6P055_HUMAN
ID Q6P055_HUMAN PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 RA Strausberg R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RM EMBL; BC065920; AAH65920.1; -; mRNA.
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00407; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 473;
 Best Local Similarity 96.6%; Pred. No. 1.9e-89;
 Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 242 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301
 QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYKCKVSNKALPAPIEKT 120
 DB 302 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 361
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
 DB 362 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 421
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
 DB 422 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEGLHNNHYTKSLSLSPGK 473

RESULT 14
 Q6MZQ6 HUMAN
 ID Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.
 AC Q6MZQ6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686G11190.
 GN Name=DKFZp686G11190;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Esophagus tumor;
 RG The German cDNA Consortium;
 RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
 RA Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BX640947; CAE45972.1; -; mRNA.
 DR HSSP; P01861; 1ADQ.
 DR SMR; Q6MZQ6; 20-475.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 475 AA; 52043 MW; B7BAE255A26F488E CRC64;
 Query Match 96.9%; Score 1221; DB 2; Length 475;
 Best Local Similarity 96.6%; Pred. No. 1.9e-89;
 Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 244 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
 QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYKCKVSNKALPAPIEKT 120
 DB 304 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 363
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
 DB 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 423
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
 DB 424 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEGLHNNHYTKSLSLSPGK 475

RESULT 15
 Q6N094 HUMAN
 ID Q6N094 HUMAN PRELIMINARY; PRT; 480 AA.
 AC Q6N094;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686O01196.
 GN Name=DKFZp686O01196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Esophagus tumor;
 RG The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640622; CAE45776.1; -; mRNA.
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;
 Query Match 96.9%; Score 1221; DB 2; Length 480;
 Best Local Similarity 96.6%; Pred. No. 2e-89;
 Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

249	EPKSCDKTHTCPCPAPALLGGPSVFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDDEVFK	308
61	NYVDGVEVHNKTKPREEQNSTYRVVSVLTVLRQNMNGKEYCKCKSVNKALPAPIEKT	120
309	NYVDGVEVHNKTKPREEQNSTYRVVSVLTVLRQDNLNGKEYCKCKSVNKALPAPIEKT	368
121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPT	180
369	ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPT	428
181	PVLDSVGSFPLYSKLTVDKSRWQQGNVPSGCSVMHEALHNYHQRSLSLSGK	232
429	PVLDSGSGFPLYSKLTVDKSRWQQGNVPSGCSVMHEGLHNYHQKSLSLSGK	480

Search completed: February 22, 2006, 21:37:12
Job time : 154.266 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:37:34 ; Search time 49.0155 Seconds
(without alignments)
556.619 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGVSFVPLAPSKSTSG.....MHEALHNHYQKRSLSLSPK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1729	98.0	371	1	US-08-236-311-7
2	1729	98.0	371	2	US-08-457-918-7
3	1729	98.0	371	2	US-10-157-408-7
4	1729	98.0	446	1	US-08-397-411-7
5	1729	98.0	449	1	US-08-458-516-13
6	1729	98.0	467	2	US-08-030-175-41
7	1729	98.0	467	2	US-08-030-175-42
8	1729	98.0	470	2	US-10-104-047-3730
9	1729	98.0	476	1	US-08-378-939-10
10	1729	98.0	547	2	US-09-746-359A-54
11	1729	98.0	567	2	US-09-825-561A-16
12	1729	98.0	571	2	US-09-746-359A-53
13	1729	98.0	951	2	US-09-313-942-9
14	1729	98.0	951	2	US-10-282-162-9
15	1729	97.8	462	2	US-09-289-942A-7
16	1725	97.8	475	2	US-09-740-002-27
17	1725	97.8	476	2	US-08-487-550-4
18	1725	97.8	476	2	US-08-487-550-12
19	1725	97.8	476	2	US-09-526-098-4
20	1725	97.8	476	2	US-09-526-098-12
21	1725	97.8	476	2	US-09-383-916-4
22	1725	97.8	476	2	US-09-383-916-12
23	1725	97.8	476	2	US-09-758-173-4
24	1725	97.8	476	2	US-09-758-173-12
25	1725	97.8	476	2	US-09-576-424-4
26	1725	97.8	476	2	US-09-576-424-12
27	1725	97.8	478	2	US-08-487-550-8

28	1725	97.8	478	2	US-09-526-098-8	Sequence 8, Appli
29	1725	97.8	478	2	US-09-383-916-8	Sequence 8, Appli
30	1725	97.8	478	2	US-09-758-173-8	Sequence 8, Appli
31	1725	97.8	478	2	US-09-576-424-8	Sequence 8, Appli
32	1724	97.7	459	1	US-08-157-101A-7	Sequence 7, Appli
33	1724	97.7	470	2	US-09-238-741-4	Sequence 4, Appli
34	1724	97.7	475	2	US-09-740-002-25	Sequence 25, Appl
35	1723	97.7	330	2	US-09-301-593-22	Sequence 22, Appl
36	1723	97.7	451	1	US-08-887-352B-14	Sequence 14, Appl
37	1723	97.7	451	1	US-08-887-352B-16	Sequence 16, Appl
38	1723	97.7	451	1	US-08-887-352B-18	Sequence 18, Appl
39	1723	97.7	451	2	US-08-466-151-65	Sequence 65, Appl
40	1723	97.7	451	2	US-09-109-207C-14	Sequence 14, Appl
41	1723	97.7	451	2	US-09-109-207C-16	Sequence 16, Appl
42	1723	97.7	451	2	US-09-109-207C-18	Sequence 18, Appl
43	1723	97.7	451	2	US-09-282-505-2	Sequence 2, Appli
44	1723	97.7	451	2	US-09-054-255-2	Sequence 2, Appli
45	1723	97.7	451	2	US-09-296-005-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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US-08-236-311-7
Query Match          98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 42 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 101
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKHTHTCCPCAPPELLGG 120
DB 102 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKHTHTCCPCAPPELLGG 161
QY 121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 162 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 221
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 222 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 341
QY 301 QQGNVFSCSVMHAEALHNHYQORSLSLSPGK 330
DB 342 QQGNVFSCSVMHAEALHNHYQORSLSLSPGK 371

RESULT 2
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.

US-08-236-311-7
Query Match          98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 42 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 101
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKHTHTCCPCAPPELLGG 120
DB 102 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKHTHTCCPCAPPELLGG 161
QY 121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 162 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 221
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 222 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 341
QY 301 QQGNVFSCSVMHAEALHNHYQORSLSLSPGK 330
DB 342 QQGNVFSCSVMHAEALHNHYQORSLSLSPGK 371

RESULT 3
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
```



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; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1998
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7

Query Match          98.0%; Score 1729; DB 2; Length 371;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 60
DB 42 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 101
QY 61 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKKVPEPKSCKDTHTCPPCPAPPELLGG 120
DB 102 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKKVPEPKSCKDTHTCPPCPAPPELLGG 161
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 180
DB 162 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 221
QY 181 STYRVSVVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
DB 222 STYRVSVVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 341
QY 301 QQGNVFCSCVMHEALHNNHYQKSLSPGK 330
DB 342 QQGNVFCSCVMHEALHNNHYQKSLSPGK 371

RESULT 4
US-08-397-411-7
; Sequence 7, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-411-7

Query Match          98.0%; Score 1729; DB 2; Length 446;
Best Local Similarity 97.9%; Pred. No. 1.5e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 60
DB 117 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 176
QY 61 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKKVPEPKSCKDTHTCPPCPAPPELLGG 120
DB 177 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKKVPEPKSCKDTHTCPPCPAPPELLGG 236
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 180
DB 237 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 296
QY 181 STYRVSVVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
DB 297 STYRVSVVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 356
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 357 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 416
QY 301 QQGNVFCSCVMHEALHNNHYQKSLSPGK 330
DB 417 QQGNVFCSCVMHEALHNNHYQKSLSPGK 446

RESULT 5
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 577085
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

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;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/458,516
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/059,159
;; FILING DATE: 03-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-37-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 449 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-516-13

Query Match 98.0%; Score 1729; DB 1; Length 449;
Best Local Similarity 97.9%; Pred. No. 1.5e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 60
DB 120 ASTKGPSVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 179

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
DB 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 239

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 240 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 299

QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 300 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 359

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 300
DB 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 419

QY 301 QQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 330
DB 420 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 449

RESULT 6
US-08-030-175-41
; Sequence 41, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.

;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
;; COMPUTER: IBM AT compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
;; SOFTWARE: WordPerfect 5.0 (Dos Text)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/030,175
;; FILING DATE: 17-MAY-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB91/01578
;; FILING DATE: 13-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ernst, Barbara G.
;; REGISTRATION NUMBER: 30,377
;; REFERENCE/DOCKET NUMBER: 1768-113
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)783-6040
;; TELEFAX: (202)783-6031
;; INFORMATION FOR SEQ ID NO: 41:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 467 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-030-175-41

Query Match 98.0%; Score 1729; DB 2; Length 467;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 60
DB 138 ASTKGPSVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 197

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
DB 198 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 257

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 317

QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 318 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 467

RESULT 7
US-08-030-175-42
; Sequence 42, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.

COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
COMPUTER: IBM AT compatible
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
SOFTWARE: WordPerfect 5.0 (Dos Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01578
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-030-175-42

Query Match 98.0%; Score 1729; DB 2; Length 467;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSVVTVFSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCPCPAPPELLGG 120
DB 198 GLYSLSVVTVFSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCPCPAPPELLGG 257
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 258 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317
QY 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 318 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 437
QY 301 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 330
DB 438 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 467

RESULT 8
US-10-104-047-3730
Sequence 3730, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3730

LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3730
Query Match 98.0%; Score 1729; DB 2; Length 470;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSVVTVFSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCPCPAPPELLGG 120
DB 201 GLYSLSVVTVFSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCPCPAPPELLGG 260
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 261 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 320
QY 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 321 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 440
QY 301 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 330
DB 441 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 470

RESULT 9
US-08-378-939-10
Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid

QY 301 QQGNVFCSCVMHEALHNNHYQORSLSPGK 330
Db 538 QQGNVFCSCVMHEALHNNHYTKSLSPGK 567

RESULT 12

US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia B.

; TITLE OF INVENTION: Method for Treating Inflammation

; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 53

; LENGTH: 571

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-746-359A-53

Query Match 98.0%; Score 1729; DB 2; Length 571;
Best Local Similarity 97.9%; Pred. No. 2.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Db 242 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 301

QY 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPPELLGG 120
Db 302 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPPELLGG 361

QY 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNVTKPREEQYN 180
Db 362 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNVTKPREEQYN 421

QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
Db 422 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 481

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 300
Db 482 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 541

QY 301 QQGNVFCSCVMHEALHNNHYQORSLSPGK 330
Db 542 QQGNVFCSCVMHEALHNNHYTKSLSPGK 571

RESULT 13

US-09-313-942-9
; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-9

Query Match 98.0%; Score 1729; DB 2; Length 951;
Best Local Similarity 97.9%; Pred. No. 4.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Db 622 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 681

QY 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPPELLGG 120
Db 682 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPPELLGG 741

QY 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNVTKPREEQYN 180
Db 742 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNVTKPREEQYN 801

QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
Db 802 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 861

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 300
Db 862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 921

QY 301 QQGNVFCSCVMHEALHNNHYQORSLSPGK 330
Db 922 QQGNVFCSCVMHEALHNNHYTKSLSPGK 951

RESULT 14

US-10-282-162-9
; Sequence 9, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-9

Query Match 98.0%; Score 1729; DB 2; Length 951;
Best Local Similarity 97.9%; Pred. No. 4.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db |||||||
Qy 622 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 681
Db |||||||
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 120
Db |||||||
Qy 682 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 741
Db |||||||
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db |||||||
Qy 742 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 801
Db |||||||
Qy 181 STYRWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOQVYTLPPSRDE 240
Db |||||||
Qy 802 STYRWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOQVYTLPPSRDE 861
Db |||||||
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db |||||||
Qy 862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 921
Db |||||||
Qy 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db |||||||
Qy 922 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 951
Db |||||||
```

RESULT 15

US-09-289-942A-7

; Sequence 7, Application US/09289942A

; Patent No. 6482928

; GENERAL INFORMATION:

; APPLICANT: Pai, Emil F.

; APPLICANT: Klein, Michel H.

; APPLICANT: Chong, Pele

; APPLICANT: Pedyczak, Arthur

; TITLE OF INVENTION: Fab'-EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING

; TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5

; FILE REFERENCE: 1038-926 MIS:jb

; CURRENT APPLICATION NUMBER: US/09/289,942A

; CURRENT FILING DATE: 1999-04-13

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 7

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-289-942A-7

Query Match

Best Local Similarity 97.8%; Score 1725; DB 2; Length 462;

Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db |||||||
Qy 133 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 192
Db |||||||
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 120
Db |||||||
Qy 193 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 252
Db |||||||
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db |||||||
Qy 253 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 312
Db |||||||
Qy 181 STYRWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOQVYTLPPSRDE 240
Db |||||||
Qy 313 STYRWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOQVYTLPPSRDE 372
Db |||||||
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db |||||||
Qy 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 432
Db |||||||
Qy 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db |||||||
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:11 ; Search time 216.58 Seconds
(without alignments)
669.475 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNYQORSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1764	100.0	330	AA019664	AA019664 Human Igg
2	1732	98.2	330	ADZ69628	ADZ69628 Human Igg
3	1729	98.0	330	AAB04071	AAB04071 Zcytor 10
4	1729	98.0	330	AA047856	AA047856 Human Igg
5	1729	98.0	330	AAE21960	AAE21960 Human Igg
6	1729	98.0	330	ABB81641	ABB81641 Human Igg
7	1729	98.0	330	ABB05736	ABB05736 Human Igg
8	1729	98.0	330	ABP71856	ABP71856 Human Igg
9	1729	98.0	330	AAE32915	AAE32915 Human Igg
10	1729	98.0	330	AAE32627	AAE32627 Human Igg
11	1729	98.0	330	ABR82103	ABR82103 Human Igg
12	1729	98.0	330	AA031102	AA031102 Human Igg
13	1729	98.0	330	ABR55836	ABR55836 Anti-Ang-
14	1729	98.0	330	AA030893	AA030893 Human Igg
15	1729	98.0	330	ADF11389	ADF11389 Anti-OPGL
16	1729	98.0	330	ADZ97351	ADZ97351 Human Igg
17	1729	98.0	330	ADF83605	ADF83605 Cytokine
18	1729	98.0	330	ADF75001	ADF75001 Human Igg
19	1729	98.0	330	ADM41537	ADM41537 Anti-inte
20	1729	98.0	330	ADM68911	ADM68911 Human Igg
21	1729	98.0	330	ADR43460	ADR43460 Heavy cha
22	1729	98.0	330	ADR31605	ADR31605 Human Igg
23	1729	98.0	330	ADZ97909	ADZ97909 Anti-IFN-
24	1729	98.0	330	ADN33230	ADN33230 IgG1-CH h

25	1729	98.0	330	8	ADS94906	Adz94906 Anti-IFN-
26	1729	98.0	330	8	ADS33009	Adz33009 Human Igg
27	1729	98.0	330	8	ADT88869	Adt88869 Human Igg
28	1729	98.0	330	8	ADT51577	Adt51577 Heavy cha
29	1729	98.0	330	8	ADT51581	Adt51581 Heavy cha
30	1729	98.0	330	8	ADT51724	Adt51724 Human Igg
31	1729	98.0	330	8	ADU68015	Adu68015 Mouse ant
32	1729	98.0	330	8	ADW08868	Adw08868 IGF-IR an
33	1729	98.0	330	9	ADW86657	Adw86657 Human imm
34	1729	98.0	330	9	ADX97894	Adx97894 Human Igg
35	1729	98.0	330	9	ADX98273	Adx98273 Human ant
36	1729	98.0	330	9	ADY51253	Ady51253 Human Igg
37	1729	98.0	330	9	ADY58147	Ady58147 Human Igg
38	1729	98.0	330	9	ADY26687	Ady26687 Human Igg
39	1729	98.0	330	9	AEA12531	Aea12531 Human Igg
40	1729	98.0	330	9	AEA25942	Aea25942 Human imm
41	1729	98.0	330	9	AEA48148	Aea48148 Human Igg
42	1729	98.0	330	9	AE86186	Aeb86186 Amino aci
43	1729	98.0	330	9	AEC08181	Aec08181 Heavy cha
44	1729	98.0	332	8	ADL35095	Adl35095 Human Igg
45	1729	98.0	332	9	ADW07455	Adw07455 Human Igg

ALIGNMENTS

RESULT 1

AA019664

ID AA019664 standard; protein; 330 AA.

XX AC AA019664;

XX DT 28-MAR-2003 (first entry)

XX DE Human IgG1 heavy chain constant region.

XX KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
KW antitachmatic; antiallergic; antiinflammatory; dermatological;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.

XX OS Homo sapiens.

XX PN WO200288317-A2.

XX PD 07-NOV-2002.

XX PF 01-MAY-2002; 2002WO-US013527.

XX PR 01-MAY-2001; 2001US-00847208.

XX XX 24-OCT-2001; 2001US-00000439.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Saxon A, Zhang K, Zhu D;

XX DR WPI; 2003-103456/09.

XX PT New fusion molecules comprising polypeptide sequences that bind to IgG
inhibitory receptor and native IGE receptor, useful for treating Ige-
mediated hypersensitivity reactions, e.g. asthma or allergies, or
autoimmune diseases.

XX PS Claim 64; Fig 2; 116pp; English.

XX CC The present invention relates to a fusion molecule comprising a first
polypeptide sequence capable of specific binding to a native Igg
inhibitory receptor consisting of an immune receptor tyrosine-based
inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
functionally connected to a second polypeptide sequence capable of
specific binding directly or indirectly to a native Ige receptor
(Fc epsilon receptor). Also provided are nucleotide sequences encoding such a
fusion protein. The fusion molecules and compositions are useful for

CC treating an IgE-mediated biological response, preferably an IgE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgG1
CC heavy chain constant region
XX
SQ Sequence 330 AA;
Query Match 100.0%; Score 1764; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 4.6e-125;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Qy 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 120
Qy 121 PSVFLPPPKKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVSVSLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVMHGALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMHGALHNHYQOQSLSLSPGK 330
RESULT 2
ID ADZ69628 standard; protein; 330 AA.
XX
AC ADZ69628;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human IgG1 heavy chain constant region, mutant L314M.
XX
KW Heavy chain constant region; antibody engineering; protein engineering;
KW immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasm;
KW autoimmune disease; immunosuppressive; immune disorder.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 197
FT /note= "Wild-type Leu substituted by Met"
XX
FN WO2005037867-A1.
XX
PD 28-APR-2005.
XX
PF 15-OCT-2004; 2004WO-US034440.
XX
PR 15-OCT-2003; 2003US-0511687P.
PR 14-APR-2004; 2004US-0562627P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Hinton PR, Tsurushita N;

XX WPI; 2005-315683/32.
DR
XX New modified Fc-fusion protein where at least one amino acid residue from
PT the heavy chain constant region, useful for studying protein function in
PT vitro and in vivo and as potential therapeutic and diagnostic agents.
XX
PS Claim 21; SEQ ID NO 29; 170pp; English.
XX
CC The invention relates to a modified Fc-fusion protein where at least one
CC amino acid residue from the heavy chain constant region selected from
CC residues 250, 314, and 428 (Kabat numbering) is different from that
CC present in the unmodified Fc-fusion protein. Also included are an Fc-
CC fusion protein comprising an Fc region substantially identical to that of
CC a naturally occurring class IgG antibody, a modified Fc-fusion protein
CC with an in vivo mean elimination half-life at least about 1.3-fold longer
CC than that of the corresponding unmodified Fc-fusion protein, a modified
CC IgG class antibody fragment (comprising a heavy chain constant region or
CC Fc-region where at least one amino acid residue selected from the group
CC consisting of residues 250, 314, and 428 is different from that present
CC in the unmodified IgG class antibody), an isolated polynucleotide
CC molecule encoding a polypeptide comprising a sequence at least 90%
CC identical to a sequence selected from ADZ69600-ADZ69656, an isolated
CC polypeptide comprising an amino acid sequence at least 90% identical to a
CC sequence selected from ADZ69600-ADZ69656, a method for altering FcRn
CC binding affinity/serum half-life of an Fc-fusion protein (comprising
CC selecting at least one amino acid residue as cited above, and
CC substituting the selected residue(s) with an amino acid different from
CC that present in the Fc-fusion protein) and a method of producing a
CC modified Fc-fusion protein with an altered binding affinity for
CC FcRn/alterd serum half-life as compared with the unmodified Fc-fusion
CC protein (comprising preparing an expression vector comprising a suitable
CC promoter operably linked to DNA encoding at least a constant region of an
CC IgG heavy chain, transforming host cells with the vector and culturing
CC the transformed host cells to produce the modified IgG Fc fusion
CC protein). The modified antibody has a higher affinity for FcRn at pH 6.0
CC than at pH 8.0. The fusion proteins are useful for studying protein
CC function in vitro and in vivo and as potential therapeutic and diagnostic
CC agents. The present sequence represents a human IgG1 heavy chain constant
CC region with an amino acid substitution at residue 250, 314 or 428 (Kabat
CC numbering, the actual residue that is mutated is covered in the feature
CC table).
XX
SQ Sequence 330 AA;
Query Match 98.2%; Score 1732; DB 9; Length 330;
Best Local Similarity 98.2%; Pred. No. 1.2e-122;
Matches 324; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Qy 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 120
Qy 121 PSVFLPPPKKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVSVSLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVMHGALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMHGALHNHYQOQSLSLSPGK 330

RESULT 3
 AAB04071
 ID AAB04071 standard; protein; 330 AA.
 XX
 AC AAB04071;
 XX
 DT 11-APR-2001 (first entry)
 XX
 DE Zcytor 10::IGG gamma fusion peptide.
 XX
 KW zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
 KW binding; detection; modulation; recombinant cell; haematopoietic cell;
 KW lymphoid cell; myeloid cell; lymph; immune system; blood; bone;
 KW inflammatory response; inflammation; spleen; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200068381-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 11-MAY-2000; 2000WO-US012924.
 XX
 PR 11-MAY-1999; 99US-00309861.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Foster DC, Hammond AK, Lok S;
 XX
 DR WPI; 2001-016096/02.
 DR N-PSDB; AAA54473.
 XX
 PT New cytokine receptor mouse zcytor 10, useful for detecting ligands that
 PT stimulate proliferation or development of hematopoietic, lymphoid and
 PT myeloid cells.
 XX
 PS Example 17; Page 120-121; 134pp; English.
 XX
 CC Isolating a nucleotide which encodes the zcytor 10 cytokine receptor
 CC enables the production of recombinant cells expressing the receptor.
 CC Those cells can then be used to detect the presence of a modulator of
 CC zcytor10 protein by culturing the cells in the presence of a test ligand
 CC and comparing levels of activity of mouse zcytor10 in the presence and
 CC absence of the test sample. Similarly, detection of zcytor10 receptor
 CC ligand within a test sample can be achieved. The method comprising
 CC contacting a test sample containing an amino acid sequence from Cys15 or
 CC Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the
 CC binding of the polypeptide to a ligand in the sample. Specified peptide
 CC fragments of the zcytor 10 cytokine receptor and the methods described
 CC are used to identify ligands that stimulate the proliferation and/or
 CC development of haematopoietic, lymphoid and myeloid cells. Peptide
 CC fragments of the cytokine receptor are useful for treating lymphoid,
 CC immune, inflammatory, splenic, blood or bone disorders and for generating
 CC antibodies directed against the receptor. A vector expressing a secreted
 CC human zcytor 10 heterodimer is constructed. In this construct the
 CC extracellular cytokine binding domain of zcytor 10 is fused to the heavy
 CC chain of Igg gamma and the extracellular portion of the heteromeric
 CC cytokine receptor subunit (an interleukin receptor subunit) is fused to
 CC human kappa light chain (See GENESEQ record AAA54474). The two sequences
 CC are fused together using two primers (AAA54475, AAA54476)
 XX
 SQ Sequence 330 AA;
 Query Match 98.0%; Score 1729; DB 4; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASTKGPSVPLAPSSKSGTAAALGCLVKDYKPEPVTVSWNSGALTSGVHPFPAVLQSS 60
 DB 1 ASTKGPSVPLAPSSKSGTAAALGCLVKDYKPEPVTVSWNSGALTSGVHPFPAVLQSS 60

61 GLYSLSVVTVVSSSLGTQTYICNVNHPKSNTPKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
 |||||
 61 GLYSLSVVTVVSSSLGTQTYICNVNHPKSNTPKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
 |||||
 121 PSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 |||||
 121 PSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 |||||
 181 STYRVVSVLTVLHQNMMGKEYCKVSNKALPAPIETKISKAKVOPREPVVTLPPSRDE 240
 |||||
 181 STYRVVSVLTVLHQNMMGKEYCKVSNKALPAPIETKISKAKVOPREPVVTLPPSRDE 240
 |||||
 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 |||||
 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 |||||
 301 QQGNVPSVSMHEALHNHYQRRSLSLSPGK 330
 |||||
 301 QQGNVPSVSMHEALHNHYQRRSLSLSPGK 330
 |||||

RESULT 4
 AAM47856
 ID AAM47856 standard; protein; 330 AA.
 XX
 AC AAM47856;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Human Ig-gammal heavy chain constant region amino acid sequence.
 XX
 KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 KW transgenic plant.
 XX
 OS Homo sapiens.
 XX
 PN WO200183529-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 28-APR-2001; 2001WO-US013932.
 XX
 PR 28-APR-2000; 2000US-0200298P.
 XX
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.
 XX
 PI Larrick JW, Wycoff KL;
 XX
 DR WPI; 2002-041481/05.
 DR N-PSDB; ABA05265.
 XX
 PT Immunoadhesin for treating human rhinovirus infection comprises chimeric
 PT intercellular adhesion molecule-1, and optionally a J chain and secretory
 PT component in association.
 XX
 PS Disclosure; Fig 7; 138pp; English.
 XX
 CC The invention relates to an immunoadhesin comprising: (a) a chimeric
 CC intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor
 CC protein linked to at least a portion of an immunoglobulin heavy chain;
 CC and (b) optionally a J chain and secretory component associated with the
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-associated
 CC glycosylation and virucide activity. The immunoadhesin is useful for
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding
 CC sites, interfering with virus entry or uncoating and directing premature
 CC release of viral RNA and formation of empty capsids. Expression of the
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.
 CC Immunoadhesin having multiple binding sites have a higher effective
 CC affinity for the virus, thereby increasing the effectiveness of the
 CC immunoadhesin. Association of secretory component and immunoglobulin J

CC chain increases the stability of the immunoadhesin in the mucosal
CC environment. Production is significantly less expensive in plants than in
CC animal cell culture and production in plants is safer for human use,
CC since plants are not known to harbor any animal viruses. The present
CC sequence is that of a human immunoglobulin protein sequence, useful to
CC the invention
XX
XX
SQ

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
Db 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELLGG 120
Qy 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVFNHVNKTPRREQYN 180
Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVFNHVNKTPRREQYN 180
Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
Qy 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330

RESULT 5

AAE21960
ID AAE21960 standard; protein; 330 AA.

AC AAE21960;

XX 25-JUL-2002 (first entry)

DT Human death domain containing receptor (DR6) protein-related protein.

DE Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;
KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
KW adult respiratory distress syndrome; ARDS; cycostatic; thyromimetic;
KW dermatological; hepatotropic; antibacterial.

XX Homo sapiens.

XX WO200185209-A2.

XX 15-NOV-2001.

XX 30-APR-2001; 2001WO-US011735.

XX 10-MAY-2000; 2000US-0203015P.

XX (ELIL) LILLY & CO ELI.

XX Heuer JG, Liu J, Na S, Song HY, Yang D;

XX

DR WPI; 2002-351283/38.

XX Treating or preventing T cell or Th2 cell mediated condition e.g., asthma
PT or multiple sclerosis in mammal, comprises administering composition
PT comprising death domain containing receptor, DR6 agonist or antagonist.
XX
XX
PS Disclosure; Page 132-133; 133pp; English.

XX The invention relates to a method for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. The
CC method comprising administering to the mammal a pharmaceutical
CC composition comprising a death domain containing receptor (DR6) agonist
CC or antagonist. The method is useful for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6
CC agonist is useful in the manufacture of a medicament for treating or
CC preventing at least one symptom associated with aberrant apoptosis, graft
CC -versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy,
CC inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-
CC dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's
CC thyroiditis, Graves disease, transplant rejection, systemic lupus
CC erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune
CC infertility, Behcet's disease, autoimmune gastritis, fibrosing lung
CC disease, organ rejection after transplantation, thrombotic
CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
CC for treating or preventing at least one symptom associated with
CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
CC infection, complications of infection, human immunodeficiency virus
CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
CC C, autoimmune hepatitis, chronic hepatitis B, chronic cirrhosis, H. pylori
CC associated ulceration, cytoprotection during cancer treatment,
CC recuperation from chemotherapy, recuperation from irradiation therapy, or
CC a condition or symptom related to the above mentioned diseases in a
CC mammal. The present sequence is human DR6 protein-related protein

XX Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
Db 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELLGG 120
Qy 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVFNHVNKTPRREQYN 180
Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVFNHVNKTPRREQYN 180
Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
Qy 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330

RESULT 6

ABB81641
ID ABB81641 standard; protein; 330 AA.

XX AC ABB81641;
 XX DT 25-SEP-2002 (first entry)
 XX DE Human IgG gamma 1 heavy chain SEQ ID NO:15.
 XX KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
 KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
 KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
 KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
 KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;
 KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;
 KW mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis;
 KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
 KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
 KW emphysema; chronic airway disease.
 XX OS Homo sapiens.
 XX PN WO200244209-A2.
 XX PD 06-JUN-2002.
 XX PF 28-NOV-2001; 2001WO-US044808.
 XX PR 28-NOV-2000; 2000US-0253561P.
 XX PR 07-FEB-2001; 2001US-0267211P.
 XX PR (ZYMO) ZYMOGENETICS INC.
 XX PA Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;
 XX WPI: 2002-527700/56.
 XX DR N-PSDB; ABQ73076.
 XX PT Novel Zcytor19 polypeptides and polynucleotides useful for stimulating
 PT immune responses in animals for producing antibodies, and for treating
 PT autoimmune diseases, leukemia and asthma.
 XX PS Example 7; Page 171-172; 200pp; English.
 XX CC The present invention describes an isolated human zcytor19 protein (I),
 CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
 CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
 CC antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic
 CC activities, and can be used in vaccines. (I) or an antibody binding (I)
 CC can be used for suppressing the immune system for reducing rejection of
 CC tissue or organ transplants and grafts and for treating T-cell specific
 CC leukaemias or lymphomas and autoimmune diseases including rheumatoid
 CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel
 CC disease and Crohn's disease. The antibodies can also be used for treating
 CC immunologic renal diseases, glomerulonephritis, mesangioproliferative
 CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
 CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
 CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the
 CC antibodies can also be used for renal or urological neoplasms and
 CC multiple myelomas, asthma, bronchitis, emphysema and other chronic airway
 CC diseases. Human zcytor19 is located to chromosome 1, more specifically to
 CC chromosome 1p36.11. The present sequence represents a human IgG gamma 1
 CC heavy chain protein, which is used in an example from the present
 CC invention
 XX SQ Sequence 330 AA;
 XX Query Match 98.0%; Score 1729; DB 5; Length 330;
 XX Best Local Similarity 97.9%; Pred. No. 2e-122;
 XX Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 XX 1 ASTKGSPVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60
 XX 1 ASTKGSPVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60

61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
 121 PSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 121 PSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 181 STYRVSVLTVLHQNMMNGKVKCKSNKALPAPLEKTIISKAKVQPREPQVVTLPSPSRDE 240
 181 STYRVSVLTVLHQNMMNGKVKCKSNKALPAPLEKTIISKAKVQPREPQVVTLPSPSRDE 240
 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVSGSFYLSKLTVDKSRW 300
 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVSGSFYLSKLTVDKSRW 300
 301 QQGNVFSCSVMEALHNHYQQRSLSPGK 330
 301 QQGNVFSCSVMEALHNHYQQRSLSPGK 330

RESULT 7
 ABB05736
 ID ABB05736 standard; protein; 330 AA.
 XX AC ABB05736;
 XX DT 01-MAY-2002 (first entry)
 XX DE Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
 XX KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.
 XX OS Homo sapiens.
 XX PN WO200200721-A2.
 XX PD 03-JAN-2002.
 XX PF 26-JUN-2001; 2001WO-US020484.
 XX PR 26-JUN-2000; 2000US-0214282P.
 XX PR 29-JUN-2000; 2000US-0214955P.
 XX PR 08-FEB-2001; 2001US-0267963P.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
 PI Maurer MF;
 XX WPI: 2002-090519/12.
 XX N-PSDB; ABA93797.
 XX PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX PS Example 17; Page 187-188; 235pp; English.
 XX CC The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral

CC infections. They are also useful for inducing cytotoxicity and for
CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93943 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention

XX SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 5; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTRYKDKVEPKSCDKHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTRYKDKVEPKSCDKHTCCPCPAPELLGG 120
Qy 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 8
ABP71856
ID ABP71856 standard; protein; 330 AA.
XX
AC ABP71856;
XX
DT 17-APR-2003 (first entry)
XX
DE Human IgG1 Fc gamma region.
XX
KW Human; fusion protein; IgE Fc epsilon; IgG Fc gamma; Fc epsilon; allergy;
KW Fc epsilon; Fc gamma; protein therapy; IgE; IgG; asthma; hay fever;
KW allergic asthma; allergic rhinitis; hay fever; food allergy;
KW atopic dermatitis; drug allergy; peanut allergen.
XX
OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Region 1. .98
FT Region /label= CH1 region
FT Region 99. .113
FT Region /label= Hinge region
FT Region 114. .223
FT Region /label= CH2 region
FT Region 224. .330
FT Region /label= CH3 region
XX WO2002102320-A2.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-US019448.
XX

PR 15-JUN-2001; 2001US-0298710P.
XX (TANO-) TANOX INC.
XX
PI An L, Wu H, Fung MSC;
XX WPI; 2003-167440/16.
XX
PT New fusion protein which binds to Fc epsilonRI or RII receptor and
PT Fc gammaRIIb receptor, useful for treating or preventing allergies and
PT asthma, comprises an IgE Fc epsilon fragment and an IgG Fc gamma fragment.
XX
PS Disclosure; Fig 5; 32pp; English.
XX
CC The invention relates to a novel fusion protein comprising an IgE
CC Fc epsilon fragment and an IgG Fc gamma fragment, which binds to an
CC Fc epsilonRI and/or Fc epsilonRII receptor and an Fc gammaRIIb receptor. The
CC fusion protein of the invention may have a use in protein therapy. The
CC fusion protein is useful in treating or preventing IgE-mediated allergies
CC and asthma, such as allergic asthma, allergic rhinitis, hay fever, food
CC allergy, atopic dermatitis and drug allergy. The allergic response is
CC particularly caused by peanut allergen. The present sequence represents
CC the human IgG1 Fc gamma fragment
XX
SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTRYKDKVEPKSCDKHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTRYKDKVEPKSCDKHTCCPCPAPELLGG 120
Qy 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 9
AAE32915
ID AAE32915 standard; protein; 330 AA.
XX
AC AAE32915;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.
XX
KW T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.
XX
OS Homo sapiens.
XX
PN WO200279232-A2.
XX
PD 10-OCT-2002.
XX

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PF 30-MAR-2002; 2002WO-US009815.
XX
PR 30-MAR-2001; 2001US-0280625P.
XX
PA (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD;
XX
DR WPI; 2003-103259/09.
XX
XX
PT Reducing the immunogenicity of a fusion protein comprises changing an
PT amino acid within the junction region to reduce the ability of the
PT candidate T-cell epitope identified within the junction spanning to
PT interact with T-cell receptor.
XX
XX Disclosure; Page 49-50; 68pp; English.
XX
XX The invention relates to a method for reducing the immunogenicity of a
XX fusion protein which involves identifying a candidate T-cell epitope
XX within a junction spanning a fusion junction of a fusion protein, and
XX changing an amino acid within the junction region to reduce the ability
XX of the candidate T-cell epitope to interact with a T-cell receptor. The
XX method is useful for reducing the immunogenicity of a fusion protein. It
XX is useful for analysing, changing or modifying one or more amino acids in
XX the junction region of a fusion protein to identify a T-cell epitope and
XX reduce its ability to interact with a T-cell receptor. The less
XX immunogenic fusion proteins are useful in providing therapeutic
XX treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy
XX chain Fc region used to illustrate the method of the invention
XX
SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGSPVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGSPVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSIGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSIGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVHMEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVHMEALHNHYTQKSLSLSPGK 330
RESULT 10
AAE32627
ID AAE32627 standard; protein; 330 AA.
XX
AC AAE32627;
XX
XX 24-MAR-2003 (first entry)
XX
XX Human immunoglobulin G1 (IgG1) heavy chain Fc region.
XX
XX Human; immunogenic; therapy; immunoglobulin G1; IgG1.
XX
```

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OS Homo sapiens.
XX
PN WO200279415-A2.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-US009650.
XX
XX 30-MAR-2001; 2001US-0280625P.
XX
XX (LEXI-) LEXIGEN PHARM CORP.
XX
XX Gillies SD;
XX
XX WPI; 2003-111794/10.
XX
XX Reducing the immunogenicity of a fusion protein by changing an amino acid
XX within the junction region spanning a fusion junction of a fusion protein
XX to reduce the ability of the candidate T-cell epitope to interact with a
XX T-cell receptor.
XX
XX Disclosure; Page 49-50; 67pp; English.
XX
XX The present invention relates to a method of reducing the immunogenicity
XX of a fusion protein. The method involves identifying a candidate T-cell
XX epitope within a junction region spanning a fusion junction of a fusion
XX protein and changing an amino acid within the junction region to reduce
XX the ability of the candidate T-cell epitope to interact with a T-cell
XX receptor. The method is useful for reducing the immunogenicity of fusion
XX proteins for use in therapy. The present sequence is human immunoglobulin
XX G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the
XX method of the invention
XX
SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGSPVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGSPVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSIGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSIGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVHMEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVHMEALHNHYTQKSLSLSPGK 330
RESULT 11
ABR82103
ID ABR82103 standard; protein; 330 AA.
XX
XX ABR82103;
XX
XX 23-SEP-2003 (first entry)
XX
XX Human DR6 related amino acid sequence SEQ ID NO:5.
```

XX Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;
KW antiarthritic; antiasthmatic; dermatological; antiinflammatory;
KW antidiabetic; antidiabetic; cytostatic; neuroprotective; thyromimetic;
KW antihypertensive; antihypertensive; antihypertensive; virucide;
KW hepatotropic; antibacterial; antitumor; haemostatic; antianemic;
KW antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.
XX Homo sapiens.
XX WO2003051290-A2.
XX 26-JUN-2003.
XX 10-DEC-2002; 2002WO-US037596.
XX 17-DEC-2001; 2001US-0342632P.
XX (ELIL) LILLY & CO ELI.
XX Liu J, Na S, Song HY, Yang D;
XX WPI; 2003-541604/51.
XX Treating or preventing a B cell mediated condition e.g., chronic
PT hepatitis or chronic cirrhosis, in a mammal by administering a
PT pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to
PT the mammal.
XX Disclosure; Page 96-97; 97pp; English.
XX The present invention describes a method (M1) for treating or preventing
CC a B cell mediated condition in a mammal by administering a pharmaceutical
CC composition comprising a DR6 agonist or DR6 antagonist to the mammal.
CC Also described: (1) inhibiting B cell mediated immunity in a mammal, by
CC administering a pharmaceutical composition comprising at least one DR6
CC agonist; (2) use of a DR6 agonist in the manufacture of a medicament for
CC treating or preventing at least one symptom associated with conditions
CC (C1) such as aberrant apoptosis, graft-versus-host disease (GVHD), atopy,
CC rheumatoid arthritis, asthma, eczema, inflammatory bowel disease, cancer,
CC vasculitis, psoriasis, insulin-dependent diabetes mellitus, pancreatitis,
CC psoriasis, multiple sclerosis, Hashimoto's thyroiditis, Graves' disease,
CC transplant rejection, systemic lupus erythematosus, Behcet's disease,
CC autoimmune nephropathy, autoimmune haematopathy, idiopathic interstitial
CC pneumonia, hypersensitivity pneumonitis, autoimmune dermatosis,
CC autoimmune cardiopathy, autoimmune infertility, autoimmune gastritis,
CC fibrosing lung disease, fulminant viral hepatitis B, fulminant viral
CC hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
CC Helicobacter pylori-associated ulceration, organ rejection after
CC transplantation, chronic glomerulonephritis, thrombotic thrombocytopenic
CC purpura (TTP) and haemolytic uraemic syndrome (HUS), aplastic anaemia,
CC myelodysplasia, multiple organ dysfunction syndrome (MDS), adult
CC respiratory distress syndrome (ARDS), and at least one condition or
CC symptom related to the conditions, in a mammal; and (3) use of DR6
CC antagonist in the manufacture of a medicament for treating or preventing
CC at least one symptom associated with conditions (C2) such as aberrant
CC apoptosis, immunodeficiency, bacterial infection, viral infection,
CC microbial infection, complications of infection, HIV, HIV-induced
CC lymphoma, HIV-induced AIDS, fulminant viral hepatitis B, fulminant viral
CC hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
CC H. pylori-associated ulceration, cytoprotection during cancer treatment,
CC recuperation from chemotherapy, recuperation from irradiation therapy,
CC and at least one condition or symptom related to the conditions, in a
CC mammal. DR6 has immunosuppressive, antirheumatic, antiarthritic,
CC antiasthmatic, dermatological, antiinflammatory, antipsoriatic,
CC antidiabetic, cytostatic, neuroprotective, thyromimetic, antithyroid,
CC nephrotropic, antiinfertility, vasotropic, virucide, hepatotropic,
CC antibacterial, antitumor, haemostatic, antianemic, antimicrobial and
CC anti-HIV activities. (M1) is useful for treating or preventing at least
CC one symptom associated with (C1) in a mammal, preferably human, by
CC administering DR6 agonist, and for treating or preventing at least one
CC symptom associated with (C2) by administering DR6 antagonist. The present
CC sequence represents a human DR6 related amino acid sequence, which is

CC given in the exemplification of the present invention
XX
SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVEPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHPFPAVLQSS 60
DB 1 ASTKGPSVEPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHPFPAVLQSS 60
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVSVLTVLHONMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 181 STYRVSVLTVLHONMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLYSLKTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLYSLKTVDKSRW 300
QY 301 QGQNVFSCSVMEALHNNHYQQRSLSPK 330
DB 301 QGQNVFSCSVMEALHNNHYQQRSLSPK 330
RESULT 12
AAO31102
ID AAO31102 standard; protein; 330 AA.
AC AAO31102;
DT 06-OCT-2003 (first entry)
DE Human A2-G8 SCF antibody heavy chain constant region.
KW Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
KW steel factor; c-kit ligand; gene therapy; heavy chain.
OS Homo sapiens.
PN WO2003051311-A2.
PD 26-JUN-2003.
PF 16-DEC-2002; 2002WO-US040227.
PR 17-DEC-2001; 2001US-0342174P.
PA (FARB) BAYER CORP.
PI Takeuchi T, Tomkinson A, Neben S;
XX WPI; 2003-523500/49.
XX N-PSDB; AAL62618.
XX New purified human antibody that binds to stem cell factor protein,
PT useful for preparing a composition for treating asthma.
XX Example 10; Page 47-48; 94pp; English.
XX The invention provides human antibodies that bind to stem cell factor
CC (SCF) protein. SCF is also known as mast cell growth factor, steel factor
CC or c-kit ligand. Antibodies of the invention are useful for preparing
CC compositions for treating asthma. They are also used in gene therapy. The
CC present sequence is human SCF antibody heavy chain constant region

XX SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVPSSSSLGTQYICNVNHPKSNKTKVDPKSCDKTHTCPPCPAPPELLGG 120
DB 61 GLYSLSSVTVPSSSSLGTQYICNVNHPKSNKTKVDPKSCDKTHTCPPCPAPPELLGG 120
QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
RESULT 13
ID ABR55836 standard; protein; 330 AA.
XX ABR55836;
XX 02-SEP-2003 (first entry)
XX Anti-Ang-2 antibody IgG1 constant region.
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody; human.
OS Homo sapiens.
XX WO2003030833-A2.
XX 17-APR-2003.
XX 11-OCT-2002; 2002WO-US032613.
XX 11-OCT-2001; 2001US-0328604P.
PR 10-OCT-2002; 2002US-00269805.
XX (AMGE-) AMGEN INC.
XX Oliner JD;
XX WPI; 2003-504963/47.
XX New specific binding agents (i.e. anti-angiotensin-2 antibodies), useful
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX Example 4; Page 96; 161pp; English.
XX The invention relates to a specific binding agent, which comprises at
CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
CC fragment. The binding agents are antibodies that recognize and bind to
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the

CC antibody, is useful for inhibiting undesired angiogenesis, treating
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC 2 activity, modulating vascular permeability or plasma leakage, or
CC treating a disease (e.g. ocular neovascular disease, obesity,
CC haemangiomas, haemangioma, arteriosclerosis, inflammatory disease,
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a human IgG1 constant region of an anti-Ang-2
CC antibody
XX SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVPSSSSLGTQYICNVNHPKSNKTKVDPKSCDKTHTCPPCPAPPELLGG 120
DB 61 GLYSLSSVTVPSSSSLGTQYICNVNHPKSNKTKVDPKSCDKTHTCPPCPAPPELLGG 120
QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
RESULT 14
ID AAO30893 standard; protein; 330 AA.
XX AAO30893;
XX 22-SEP-2003 (first entry)
XX Human immunoglobulin gamma (IgG) 1 constant region.
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; human.
OS Homo sapiens.
XX WO2003048334-A2.
XX 12-JUN-2003.
XX 04-DEC-2002; 2002WO-US038780.
XX 04-DEC-2001; 2001US-0337113P.
PR 12-APR-2002; 2002US-0371966P.
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
XX Gillies SD;
XX WPI; 2003-513757/48.
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT moiety, useful for preparing a composition for treating cancer, viral

PT infections or immune disorders.
 XX
 PS Example 1; Page 51-53; 71pp; English.
 XX
 CC The invention relates to cytokine fusion proteins with increased
 CC therapeutic index and methods for increasing the therapeutic index of
 CC such fusion proteins. The fusion protein comprises a non-interleukin-2
 CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
 CC composition for treating cancer, viral infections or immune disorders.
 CC The fusion protein is also used in gene therapy. The present sequence is
 CC human immunoglobulin gamma (IgG) constant region. This sequence is used
 CC to illustrate the method of the invention
 XX
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Qy 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 240
 Db 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFSFLYSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFSFLYSKLTVDKSRW 300
 Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
 Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 15
 ADF11389
 ID ADF11389 standard; protein; 330 AA.
 XX
 AC ADF11389;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.
 XX
 KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
 XX
 OS Homo sapiens.
 XX
 FN WO2003086289-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 07-APR-2003; 2003WO-US010749.
 XX
 PR 05-APR-2002; 2002US-0370407P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
 XX WPI, 2003-845253/78.
 DR

DR N-PSDB; ADF11388.
 XX
 PT New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.
 XX
 XX Example 3; SEQ ID NO 2; 156pp; English.
 XX
 CC The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 7; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Qy 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 240
 Db 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFSFLYSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFSFLYSKLTVDKSRW 300
 Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
 Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

Search completed: February 22, 2006, 21:30:43
 Job time : 220.58 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:31:15 ; Search time 33.6269 Seconds
(without alignments)
944.229 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPSVFLAPSSKSTSG.....MHEALHNYQQRSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1729	98.0	330	1 GHU	Ig gamma-1 chain C
2	1592.5	90.3	377	2 A23511	Ig gamma-3 chain C
3	1590.5	90.2	377	2 A60764	Ig gamma-3 chain C
4	1566	88.8	326	1 G2HU	Ig gamma-2 chain C
5	1552.5	88.0	377	1 G4HU	Ig gamma-4 chain C
6	1225.5	69.5	374	2 S69339	Ig heavy chain V r
7	1225	69.4	328	2 I47159	Ig gamma 2a chain
8	1222	69.3	255	4 S31866	Ig gamma-1 chain C
9	1219	69.1	328	2 I47160	Ig gamma 2b chain
10	1216	68.9	234	2 PT0207	Ig gamma chain C r
11	1193	67.6	328	2 I47158	Ig gamma 1 chain C
12	1192.5	67.6	323	1 GHRB	Ig gamma chain C r
13	1189	67.4	328	2 I47161	Ig gamma 3 chain C
14	1174.5	66.6	329	1 G2GP	Ig gamma-2 chain C
15	1163.5	66.0	472	2 S31459	Ig gamma-1 chain -
16	1144.5	64.9	470	2 S22080	Ig heavy chain pre
17	1125.5	63.8	308	2 C30554	Ig heavy chain C r
18	1123	63.7	229	1 G3HUW1	Ig gamma-3 heavy c
19	1117.5	63.4	333	2 PS0018	Ig gamma-2b chain
20	1116	63.3	444	2 PC4436	monoclonal antibod
21	1114	63.2	326	2 PS0017	Ig gamma-1 chain C
22	1109	62.9	324	1 G1MS	Ig gamma-1 chain C
23	1108	62.8	329	1 G3MSC	Ig gamma-3 chain C
24	1104	62.6	333	1 G1MSM	Ig gamma-1 chain C
25	1097	62.2	398	1 G3MSM	Ig gamma-3 chain C
26	1093	62.0	330	1 G2MSA	Ig gamma-2a chain
27	1093	62.0	469	2 S37483	Ig gamma-2a chain
28	1090.5	61.8	335	1 G2MSAB	Ig gamma-2a chain
29	1088	61.7	399	1 G2MSAM	Ig gamma-2a chain

Ig gamma-2c chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma 4 chain c
Ig gamma heavy cha
Ig epsilon chain C
Ig heavy chain VHI
Ig heavy chain V-1
Ig heavy chain pre
Ig gamma-1 chain C
Ig gamma-1 heavy c
Ig heavy chain (DO

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A;Note: This sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers,

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S38861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequ

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96, 'R', 98-135 <CUN>

A;Cross-references: UNIPARC:UPI000017378D

A;Note: This sequence has the Gm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154, 'O', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240

A;Cross-references: UNIPARC:UPI000017378E

A;Note: This sequence has the Gm(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Cross-references: UNIPARC:UPI000017378F
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 Ko
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Cross-references: UNIPARC:UPI0000173790
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;247-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 98.0%; Score 1729; DB 1; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.2e-113;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60

Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVPKSCDTHTCPCPAPELLGG 120
Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVPKSCDTHTCPCPAPELLGG 120

Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180

Qy 181 STYRVSVTLVTHQNMWGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVSVTLVTHQDNLWGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

Qy 241 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVSYFLYSLKTVDKSRW 300
Db 241 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVSYFLYSLKTVDKSRW 300

Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

||||| 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
|||||
RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; MID:g33070; PIDN:CAA27.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 1592.5; DB 2; Length 377;
Best Local Similarity 80.1%; Pred. No. 4.8e-104;
Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60

Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVV----- 98
Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVELKTPGLDTHTCPRCEPKSC 120

Qy 99 -----EPKSCDKTHTCPCPAPELLGSPVFLPPKPKDT 133
Db 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPAPELLGSPVFLPPKPKDT 180

Qy 134 LMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYNSTYRVSVTLVLH 193
Db 181 LMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYNSTYRVSVTLVLH 240

Qy 194 QNMWGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 253
Db 241 QDNLWGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 300

Qy 254 GFYPSDIAVEWESNGQPENNYKTPPVLDVSGVSYFLYSLKTVDKSRWQGNVFCSCVMHE 313
Db 301 GFYPSDIAVEWESNGQPENNYKTPPVLDVSGVSYFLYSLKTVDKSRWQGNVFCSCVMHE 360

Qy 314 ALHNHYQOQSLSLSPGK 330
Db 361 ALHNRTQKLSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 conver
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA

A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176FOB
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM>
Query Match 90.2%; Score 1590.5; DB 2; Length 377;
Best Local Similarity 80.1%; Pred. No. 6.6e-104;
Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;
QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKV----- 98
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKRVELKTPGLDTHTCRCPPEKSC 120
QY 99 -----EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKPKDT 133
DB 121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPAPPELLGGPSVFLFPPPKPKDT 180
QY 134 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYNSTYRVSVLTVLH 193
DB 181 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYNSTYRVSVLTVLH 240
QY 194 QNMNGKEYCKVSKNKPAPTEKTSKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVK 253
DB 241 QWLNGKEYCKVSKNKPAPTEKTSKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVK 300
QY 254 GFYPDSIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRWQGNVFCSSVMHE 313
DB 301 GFYPDSIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRWQGNVFCSSVMHE 360
QY 314 ALNHVYQSRSLSPGK 330
DB 361 ALNHVYQSRSLSPGK 377
RESULT 4
GZHU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
A:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFPC; GB:V00554; GB:J00230; NID:932
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein rII
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', '21-57, 'Z', '59, 'A', '61-193, 'D', '195-325 <WAN>
A:Cross-references: UNIPARC:UPI0000173791
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', '26-57, 'EV', '60-85, '132-171, 'ZZZ', '175, 'B', '177-193, 'D', '195-196, 'Q', '198-
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793

A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Aclab, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:1GHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kl
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.8%; Score 1566; DB 1; Length 326;
Best Local Similarity 89.1%; Pred. No. 2.8e-102;
Matches 294; Conservative 15; Mismatches 17; Indels 4; Gaps 2;
QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 116
QY 121 PSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYN 180
DB 117 PSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYN 176
QY 181 STYRVSVLTVLHQNMMNGKEYCKVSKNKPAPTEKTSKAKVOPREPQVYTLPPSRDE 240
DB 177 STYRVSVLTVLHQNMMNGKEYCKVSKNKPAPTEKTSKAKVOPREPQVYTLPPSRDE 236
QY 241 LTKNOVSLTCLVKGYFSDIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRW 300
DB 237 MTKNOVSLTCLVKGYFSDIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRW 296
QY 301 QGNVFCSSVMHEALNHVYQSRSLSPGK 330
DB 297 QGNVFCSSVMHEALNHVYQSRSLSPGK 326

RESULT 5
G4HU

Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:93157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30,81-326 <PIN>
A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:147/Disulfide bonds: interchain (to light chain) #status experimental
F:127-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 88.0%; Score 1552.5; DB 1; Length 327;
Best Local Similarity 88.8%; Pred. No. 2.5e-101;
Matches 293; Conservative 15; Mismatches 19; Indels 3; Gaps 1;
Qy 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKGDPYPPVTVSNWNSGALTSVHTTPAVLQSS 60
Db 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKGDPYPPVTVSNWNSGALTSVHTTPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTTQYICNVNHPKSNKVDKPKSCDKHTCTPCPAPELLGG 120
Db 61 GLYSLSVTVTPSSSLGTTQYICNVNHPKSNKVDKPKSCDKHTCTPCPAPELLGG 117
Qy 121 PSVFLPPKPDTLMIISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYN 180
Db 118 PSVFLPPKPDTLMIISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQFN 177
Qy 181 STYRVSVTLVHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPQVYTLPPSRDE 240
Db 178 STYRVSVTLVHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPQVYTLPPSQEE 237
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFSLYSLKLTVDKSRW 300
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFSLYSLKLTVDKSRW 297
Qy 301 QQGNVFCSVNHEALHNHYQQRSLSPGK 330
Db 298 QEGNVFCSVNHEALHNHYTQKSLSLGLK 327
RESULT 6
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176P24; EMBL:X81695
R;Khamlichi, A.A.
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176P25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
Query Match 69.5%; Score 1225.5; DB 2; Length 374;
Best Local Similarity 87.1%; Pred. No. 2.2e-78;
Matches 230; Conservative 6; Mismatches 17; Indels 11; Gaps 2;
Qy 78 TOTYICNVN-----HK-PSNTKVDKVPKSCDKHTCTPCPAPELLGGPSVFLF 126
Db 111 TATYICGVSEGVGGYRFSHWGQGLTVTVSSEPKSCDKHTCTPCPAPELLGGPSVFLF 170
Qy 127 PPKPKDTLMIISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYNSTYRVV 186
Db 171 PPKPKDTLMIISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYNSTYRVV 230
Qy 187 SVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPQVYTLPPSRDELTKNOV 246
Db 231 SVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPQVYTLPPSRDELTKNOV 290
Qy 247 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFSLYSLKLTVDKSRWQGNVF 306
Db 291 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFSLYSLKLTVDKSRWQGNVF 350
Qy 307 SCSVMHEALHNHYQQRSLSPGK 330
Db 351 SCSVMHEALHNHYTQKSLSLSPGK 374
RESULT 7
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
C;Genetics:
A;Gene: IGG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>
Query Match 69.4%; Score 1225; DB 2; Length 328;
Best Local Similarity 67.5%; Pred. No. 2e-78;
Matches 224; Conservative 46; Mismatches 56; Indels 6; Gaps 2;
Qy 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKGDPYPPVTVSNWNSGALTSVHTTPAVLQSS 60
Db 1 APKTAPSVFLPAPCSRDTSGPNVALGCLASSYFPPEVTVTNWNSGALSSGVHTTPSVLQPS 60

QY 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKKEPKSCDKTHTCPCPAPPELLGG 120
Db 61 GLYSLSSMTVTPASSLSKSYTCNVNHPATTTTKVDKRGVTKTKPPCPICPACESP---G 116
QY 121 PSVLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 117 PSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 176
QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIETKISKAKVQPREPVYTLPPSRDE 240
Db 177 STYRVSVLPIQHQLWNGKEFKCKVNNKDLPAPIRIISKAKGQTRPQVYTLPPHAE 236
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDVSGSFYSLKLTVDKS 298
Db 237 LRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPQQDVGDTYFLYKFSVDKA 296
QY 299 RMOQGNVFSCSVMHAEALHNNHYQORSLSLSPGK 330
Db 297 SWQGGGIFQCAVMHEALHNNHYTKSISKTPGK 328
RESULT 8
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Pilpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:933068; PIDN:CAA49866.1; PII
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region
Query Match 69.3%; Score 1222; DB 4; Length 255;
Best Local Similarity 94.8%; Pred. No. 2.3e-78;
Matches 226; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
QY 92 TKVDKKEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSH 151
Db 17 TVAAQDVESKCDKTHTCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSH 76
QY 152 EDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKAL 211
Db 77 EDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKAL 136
QY 212 PAPIETKISKAKVQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 271
Db 137 PAPIETKISKAKVQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196
QY 272 NNKTTTPPVLDVSGSFYSLKLTVDKSRMOQGNVFSCSVMHAEALHNNHYQORSLSLSPGK 330
Db 197 NNKTTTPPVLDVSGSFYSLKLTVDKSRMOQGNVFSCSVMHAEALHNNHYTKSISLSPGK 255
RESULT 9
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:9433125; PIDN:AAA52218.1; P
C:Genetic:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 69.1%; Score 1219; DB 2; Length 328;
Best Local Similarity 67.2%; Pred. No. 5.2e-78;
Matches 223; Conservative 45; Mismatches 58; Indels 6; Gaps 2;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 1 APTKAPLVVPLAQCGRDTSGPNVALGCLASSYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKKEPKSCDKTHTCPCPAPPELLGG 120
Db 61 GLYSLSSMTVTPASSLSKSYTCNVNHPATTTTKVDKRGVTKTKPPCPICPACESP---G 116
QY 121 PSVLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 117 PSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 176
QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIETKISKAKVQPREPVYTLPPSRDE 240
Db 177 STYRVSVLPIQHQLWNGKEFKCKVNNKDLPAPIRIISKAKGQTRPQVYTLPPHAE 236
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDVSGSFYSLKLTVDKS 298
Db 237 LRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPQQDVGDTYFLYKFSVDKA 296
QY 299 RMOQGNVFSCSVMHAEALHNNHYQORSLSLSPGK 330
Db 297 SWQGGGIFQCAVMHEALHNNHYTKSISKTPGK 328
RESULT 10
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
A:Cross-references: UNIPARC:UPI0000176F05
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>
Query Match 68.9%; Score 1216; DB 2; Length 234;
Best Local Similarity 95.7%; Pred. No. 5.5e-78;
Matches 224; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 90 SNTKVDKKEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDV 149
Db 1 SNTKVDKKEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDV 60
QY 150 SHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 209
Db 61 SHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 120
QY 210 ALPAPIETKISKAKVQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 269
Db 121 ALPAPIETKISKAKVQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 180
QY 270 PENNYKTTTPPVLDVSGSFYSLKLTVDKSRMOQGNVFSCSVMHAEALHNNHYQORS 323

Db 181 PENNYKTTTPVLDSGDFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKS 234

RESULT 11
I47158
Ig gamma 1 chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47158
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B cell cDNA library
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47158
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:G433121; PIDN:AAA52216.1; PID:133-202/Domain: immunoglobulin homology <IMM>
C/Genetics:
A/Gene: IgG1
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 1193; DB 2; Length 328;
Best Local Similarity 67.2%; Pred. No. 3.4e-76;
Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVWNSGALTSVHTFPVAVLQSS 60
Db 1 AKPTAPSVFLPACGRDVGPNVAGLASSYFPPEPTVWNSGALTSVHTFPVAVLQPS 60

Qy 61 GLYSLSVWTVTPSSSLGTQYICNVAKPSNTKVDKVEPKSCDKHTCCPCAPPELLGG 120
Db 61 GLYSLSVWTVTPASSLSKSYTCNVNHPATTTKVDKRV---GIHQPTCPCGCE-VAG 116

Qy 121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 117 PSVFIFFPKPKDTLMISQTEPTVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 176

Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 177 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSAEE 236

Qy 241 LTRKQVSLTCLVKGFPYSDIAVESNGQ--PENNYKTTTPVLDSVCSFELYSLKLTVDKS 298
Db 237 LSRKSVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQDVGDTFFLYSLKLAVDKA 296

Qy 299 RWQGNVFCSCVMHEALHNHYQQRSLSLSPGK 330
Db 297 RWDHGDVFECAVMHEALHNHYTKSISKTQK 328

RESULT 12
GHRB
Ig gamma chain C region - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C/Accession: A91749; A90290; A93928; A90245; A94416; A02161
R/Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A/Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype
A/Reference number: A91749; MUID:84030930; PMID:6313520
A/Accession: A91749
A/Molecule type: mRNA
A/Residues: 1-323 <BER>
A/Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A/Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R/Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A/Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G
A/Reference number: A90290; MUID:76135469; PMID:1243651
A/Accession: A90290
A/Molecule type: protein

A/Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>
A/Cross-references: UNIPARC:UPI00001737AB
R/Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A/Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A/Reference number: A93928; MUID:83299917; PMID:6193512
A/Accession: A93928
A/Molecule type: mRNA
A/Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A/Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:G165111; PIDN:AAA31289.1; PID:133-202/Domain: immunoglobulin homology <IMM>
A/Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, 185-Ala
R/Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A/Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G
A/Reference number: A90245; MUID:70110015; PMID:5461106
A/Accession: A90245
A/Molecule type: protein
A/Residues: 132-143, 'E', 145-161 <FRU>
A/Cross-references: UNIPARC:UPI00001737AC
R/Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, 1970
A/Reference number: A94416
A/Accession: A94416
A/Molecule type: protein
A/Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', 236-303/Domain: immunoglobulin homology <IM3>
A/Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AB
A/Note: this has the e15 allotypic marker, 185-Ala
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a C superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F/20-82/Domain: immunoglobulin homology <IM1>
F/130-199/Domain: immunoglobulin homology <IM2>
F/236-303/Domain: immunoglobulin homology <IM3>
F/173/Binding site: carbohydrate (Asn) #status predicted

Query Match 67.6%; Score 1192.5; DB 1; Length 323;
Best Local Similarity 67.9%; Pred. No. 3.7e-76;
Matches 222; Conservative 37; Mismatches 61; Indels 7; Gaps 2;

Qy 4 KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVWNSGALTSVHTFPVAVLQSSGLY 63
Db 4 KAPSVFLPAPCCGDTPSSTVTILGCLVKGLPEPTVWNSGTLTNGVTFPSVRSQSGLY 63

Qy 64 SLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTCCPCAPPELLGSPV 123
Db 64 SLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTCCPCAPPELLGSPV 116

Qy 124 FLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYNSTY 183
Db 117 FLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYNSTY 176

Qy 184 RVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDELTK 243
Db 177 RVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDELTK 236

Qy 244 NQVSLTCLVKGFPYSDIAVESNGQPEPENTYRTTPPQDVGDTFFLYSLKLTVDKSRWQOG 303
Db 237 RVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDELTK 296

Qy 304 NVFSCSVMHEALHNHYQQRSLSLSPGK 330
Db 297 DVFTCSVMHEALHNHYTKSISRSPGK 323

RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47161
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:9433127; PIDN:AAA52219.1; PI
C;Genetics:
A;Gene: Igg3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 67.4%; Score 1189; DB 2; Length 328;
Best Local Similarity 66.9%; Pred. No. 6.5e-76;
Matches 222; Conservative 43; Mismatches 61; Indels 6; Gaps 3;

QY 1 ASTKGSVPFLAPSSKSTSGTAAAGCLVADYFPEPVTVSNWNGALTSVHTPPAVLQSS 60
Db 1 APTAFSVPLACGRTDTSNVALGCLASSYFPEPVTVSNWNGALTSVHTPPAVLQSS 60

QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHTCPPCPAPPELLGG 120
Db 61 GLYSLSVTVTPASSLSKSYTCNVNHPATTTKVDKXVGTKT---KPPCPICPGCB-VAG 116

QY 121 PSVFLPPPKPKDTLMTLSRTPEVTCVVDVSHEDPEVKFNWYDGVVHNWVTKKPREEQYN 180
Db 117 PSVFIFPPPKPKDTLMTLSQTPETVTCVVDVSKHAQVQSVYDGVVHTAETRPKEQFN 176

QY 181 STYRVSVLTVLHONWNGEYKCKVSNKALPAIEKTIISKAKVQPREQVYTLPPSRDE 240
Db 177 STYRVSVLPIQHQDMLKGFCKVKNVNDLPAPITRTISKATGQSRBPQVYTLPPPAEE 236

QY 241 LTKNQVSLTCLVKGFPSPDIADVWESNGQ--PENNYKTTTPPVLDVSGSPFLYSKLTVDKS 298
Db 237 LRSKVTIVCLVIGFPPDILHVNWKNQGPPEPENGRTTPPQDQVDTGTFELISKLAVDKA 296

QY 299 RMOQGNVFCVSNVHEALHNHYQORSLSLSPGK 330
Db 297 RWDHGETFECVNVHEALHNHYTKQSIKSTQCK 328

RESULT 14
G2GP
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E
R;Birstein, B.K.; Huseain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
A;Cross-references: UNIPARC:UPI000017379F
R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
A;Reference number: A90359; MUID:71058486; PMID:5538616
A;Accession: A90359
A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
A;Cross-references: UNIPARC:UPI00001737A2
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
A;Molecule type: protein
A;Residues: 227-311 <TR2>
A;Cross-references: UNIPARC:UPI00001737A3
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Content: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match 66.6%; Score 1174.5; DB 1; Length 329;
Best Local Similarity 68.2%; Pred. No. 6.8e-75;
Matches 227; Conservative 31; Mismatches 66; Indels 9; Gaps 4;

QY 1 ASTKGSVPFLAPSSKSTSGTAAAGCLVADYFPEPVTVSNWNGALTSVHTPPAVLQSS 60
Db 2 ARTTAPSVFLAASCVDITSGSMWTLGCLVKGYPPEPVTVKNWNGALTSVHTPPAVLQ-S 60

QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTH--TCPPCPAPPELL 118
Db 61 GLYSLSVTVTPSSSQKAT---CNVAHPASSTKVDKTVPEIRTPZBPCTCPKCPPENL 116

QY 119 GGPVSFLPEPKPKDTLMTLSRTPEVTCVVDVSHEDPEVKFNWYDGVVHNWVTKKPREEQ 178
Db 117 GGPVSFIFPPPKPKDTLMTLSLTPRVTCVVDVSDPEVQFTWFDNKNKPVGNAETKPRVEQ 176

QY 179 YNSTYRVSVLTVLHONWNGEYKCKVSNKALPAIEKTIISKAKVQPREQVYTLPPSR 238
Db 177 YNTTFRVESVLPVQHQDMLRGFKCKVKNKALPAIEKTIISKAGAPMPDVYTLPPSR 236

QY 239 DELTKNQVSLTCLVKGFPSPDIADVWESNGQ--ENNYKTTTPPVLDVSGSPFLYSKLTVD 296
Db 237 DELSKSKSVTCLIIINFFPADIHVWASNRVPSKEYKNTPTPIEDADSGSYFLYSKLTVD 296

QY 297 KSRMOQGNVFCVSNVHEALHNHYQORSLSLSPG 329
Db 297 KSAWDQGTVYTCVNVHEALHNHYVTKQAIKRSRSPG 329

RESULT 15
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-472 <PAR>
A:Cross-references: UNIPARC:UPI0000176FJ5; EMBL:X69797
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 66.0%; Score 1163.5; DB 2; Length 472;
Best Local Similarity 65.7%; Pred. No. 6.3e-74;
Matches 218; Conservative 40; Mismatches 71; Indels 3; Gaps 2;

Qy	1	ASTKGPSEVPLAPSSKSTSGTAALGCLVKDYPEPEPTVTSWNSGALTSGVHTTPAVLQSS	60
Db	142	ASTTPPKYIPLTSCCGDTSSIVTLGCLVSSYMPPEPTVTSWNSGALTSGVHTTPAILQSS	201
Qy	61	GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCCPPCPAPELLGG	120
Db	202	GLYSLSSVTVTPASTSCAQIFICNVVAHPSASTKYDKRVEFGCPDCKHC-RCPPPELPGG	260
Qy	121	PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN	180
Db	261	PSVFIFPPKPKDKTLTISGTPEVTCVVVDVGGDDPEVQFSWFVDNVEVRTARTKPREEQFN	320
Qy	181	STYRVSVLTIVLHONWNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE	240
Db	321	STFRVVSALPIQHODWTGCKEFCCKVNEALPAPIVRIISRTKGQAREPQVYVLAPPQEE	380
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDSDVGSFELYSKLTVDKS	298
Db	381	LSKSTLSVTCLVTGFPDYIAVEWQKNGQPESEDKYGTTSQLDADGSYFLYSRLRVDKN	440
Qy	299	RWQGNVFSCSVMHEALHNHYQRRSLSLSPGK	330
Db	441	SWQEGDTYACVMHEALHNHYTQKSISKPPGK	472

Search completed: February 22, 2006, 21:38:16
Job time : 34.6269 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:24 ; Search time 219.43 Seconds
(without alignments)
1061.041 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPSVFLAPSSKSTSG.....MHEALHNHYQQRSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1729	98.0	330	1	IGHG1_HUMAN	P01857 homo sapien
2	1729	98.0	465	2	Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	1729	98.0	469	2	Q569F4_HUMAN	Q569f4 homo sapien
4	1729	98.0	469	2	Q727P5_HUMAN	Q727p5 homo sapien
5	1729	98.0	470	2	Q725W1_HUMAN	Q725w1 homo sapien
6	1729	98.0	470	2	Q6FUA4_HUMAN	Q6fja4 homo sapien
7	1729	98.0	475	2	Q5EFE5_HUMAN	Q5efe5 homo sapien
8	1729	98.0	475	2	Q6GMW7_HUMAN	Q6gmw7 homo sapien
9	1729	98.0	476	2	Q6GMX1_HUMAN	Q6gmx1 homo sapien
10	1726	97.8	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
11	1726	97.8	472	2	Q6N089_HUMAN	Q6n089 homo sapien
12	1725	97.8	473	2	Q6P055_HUMAN	Q6p055 homo sapien
13	1725	97.8	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
14	1725	97.8	480	2	Q6N094_HUMAN	Q6n094 homo sapien
15	1725	97.8	481	2	Q6N097_HUMAN	Q6n097 homo sapien
16	1725	97.8	482	2	Q72351_HUMAN	Q72351 homo sapien
17	1722	97.6	466	2	Q6N096_HUMAN	Q6n096 homo sapien
18	1720	97.5	348	2	Q6PYX1_HUMAN	Q6pyx1 homo sapien
19	1720	97.5	478	2	Q6P181_HUMAN	Q6p181 homo sapien
20	1720	97.5	480	2	Q6P1F1_HUMAN	Q6p1f1 homo sapien
21	1718	97.4	475	2	Q6N095_HUMAN	Q6n095 homo sapien
22	1718	97.4	544	2	Q6B395_HUMAN	Q6bj95 homo sapien
23	1710	96.9	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
24	1660	94.1	475	2	Q5RE17_PONPY	Q5re17 pongo pygma
25	1592.5	90.3	518	2	Q6N030_HUMAN	Q6n030 homo sapien
26	1592.5	90.3	519	2	Q5BEM2_HUMAN	Q5ebm2 homo sapien
27	1588.5	90.1	521	2	Q8N4Y9_HUMAN	Q8n4y9 homo sapien
28	1577.5	89.4	509	2	Q8NF17_HUMAN	Q8nf17 homo sapien
29	1566	88.8	326	1	IGHG2_HUMAN	P01859 homo sapien
30	1566	88.8	417	2	Q6N093_HUMAN	Q6n093 homo sapien
31	1561	88.5	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien

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32 1552.5 88.0 327 1 IGHG4_HUMAN
33 1552.5 88.0 470 2 Q8TC63_HUMAN
34 1552 88.0 473 2 Q68CN4_HUMAN
35 1551 87.9 464 2 Q6NZU6_HUMAN
36 1543.5 87.5 476 2 Q6MZX7_HUMAN
37 1486.5 84.3 354 2 Q86TT2_HUMAN
38 1228.5 69.6 337 2 Q95M34_HORSE
39 1226 69.5 679 2 Q96PQ8_HUMAN
40 1210.5 68.6 487 2 Q65ZL2_9MURI
41 1192.5 67.6 323 1 GC_RABIT
42 1174.5 66.6 329 1 IGHG2_CANPO
43 1128 63.9 290 1 IGHG3_HUMAN
44 1117.5 63.4 333 1 GCB_RAT
45 1117.5 63.4 469 2 Q5M839_RAT

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ALIGNMENTS

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RESULT 1
IGHG1_HUMAN
ID IGHG1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP PROTEIN SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.B., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.

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Db      1  ASTKGSVPFLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY      61  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPPELLGG 120
Db      61  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPPELLGG 120
QY      121  PSVFLPPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db      121  PSVFLPPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY      181  STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
Db      181  STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
QY      241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSVGSFFLYSKLTVDKSRW 300
Db      241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSVGSFFLYSKLTVDKSRW 300
QY      301  QGQNVFSCSVMEALHNHYQQRSLSPGK 330
Db      301  QGQNVFSCSVMEALHNHYQQRSLSPGK 330

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RESULT 2

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Q6GMX6 HUMAN
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Young A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

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DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match      98.0%; Score 1729; DB 2; Length 465;
Best Local Similarity 97.9%; Pred. No. 9.3e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1  ASTKGSVPFLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 136  ASTKGSVPFLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 195
QY 61  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPPELLGG 120
Db 196  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPPELLGG 255
QY 121  PSVFLPPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 256  PSVFLPPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 315
QY 181  STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
Db 316  STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 375
QY 241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSVGSFFLYSKLTVDKSRW 300
Db 376  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSVGSFFLYSKLTVDKSRW 435
QY 301  QGQNVFSCSVMEALHNHYQQRSLSPGK 330
Db 436  QGQNVFSCSVMEALHNHYQQRSLSPGK 465

RESULT 3
Q569F4 HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE IGHL1 protein.
GN Name=IGHL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Young A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

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RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC NIH MGC Project;
RG TISSUE=Lymph;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 469;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQSS 60
DB 140 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQSS 199

QY 61 GLYSLSVVTVFSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 120
DB 200 GLYSLSVVTVFSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 259

QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 260 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 319

QY 181 STYRVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 320 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 379

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSLKTVDKSRW 300
DB 380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSLKTVDKSRW 439

QY 301 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 330
DB 440 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 469

RESULT 4
Q727P5 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -, mRNA.
DR HSSP; P01857; 1HZH.
DR SMR; Q727P5; 20-469.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 469;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQSS 60
DB 140 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQSS 199

QY 61 GLYSLSVVTVFSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 120
DB 200 GLYSLSVVTVFSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 259

QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 260 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 319

QY 181 STYRVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 320 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 379

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSLKTVDKSRW 300
DB 380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSLKTVDKSRW 439

QY 301 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 330
DB 440 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 469

RESULT 5
Q725W1 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.J. Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
Query Match 98.0%; Score 1729; DB 2; Length 470;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120
DB 201 GLYSLSSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG 260
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
QY 181 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 321 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 440
QY 301 QGQNVFSCSWMEALHNNHYQKSLSPGK 330
DB 441 QGQNVFSCSWMEALHNNHYQKSLSPGK 470
RESULT 6
Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;
Query Match 98.0%; Score 1729; DB 2; Length 470;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120
DB 201 GLYSLSSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG 260
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
QY 181 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 321 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 440

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Qy 301 OQGNVFCVSMHEALHNHYQORSLSLSPGK 330
Db 441 OQGNVFCVSMHEALHNHYTKSLSLSPGK 470

RESULT 7
QSEFES_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEFES;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gamma1 heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Belliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RL antibody T125.";
DR EMBL; AY894992; AN082028.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT CHAIN.
SQ SEQUENCE 475 AA; 52362 MW; 1367D40DC7D2859 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 475;
Best Local Similarity 97.9%; Pred. No. 9.5e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db 146 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 205

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHHTCCPPAPPELLGG 120
Db 206 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHHTCCPPAPPELLGG 265

Qy 121 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 266 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 325

Qy 181 STYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 326 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 385

Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 386 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW 445

Qy 301 OQGNVFCVSMHEALHNHYQORSLSLSPGK 330
Db 446 OQGNVFCVSMHEALHNHYTKSLSLSPGK 475

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RESULT 8

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O6GMW7_HUMAN
ID O6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC O6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Splicein;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C-integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 475;
Best Local Similarity 97.9%; Pred. No. 9.5e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db 146 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 205

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHHTCCPPAPPELLGG 120
Db 206 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHHTCCPPAPPELLGG 265

Qy 121 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 266 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 325

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QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 326 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 385
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 445
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 QQGNVFSCSVMEALHNNHYTQKSLSPGK 330
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 446 QQGNVFSCSVMEALHNNHYTQKSLSPGK 475
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
Q6GMX1 HUMAN
ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR GO: GO:0016021, C:integral to membrane, IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG.cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654, C1-set; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
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Query Match

98.0%; Score 1729; DB 2; Length 476;

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Best Local Similarity 97.9%; Pred. No. 9.6e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCTPCPAPPELLGG 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 207 GLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCTPCPAPPELLGG 266
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNKTKPREEQYN 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 267 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNKTKPREEQYN 326
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 327 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 386
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 446
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 QQGNVFSCSVMEALHNNHYTQKSLSPGK 330
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 447 QQGNVFSCSVMEALHNNHYTQKSLSPGK 476
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
```

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
 SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCEDE81076E CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 466;
 Best Local Similarity 97.6%; Pred. No. 1.5e-118;
 Matches 322; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 DB 137 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 196
 QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELGG 120
 DB 197 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELGG 256
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 DB 257 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 316
 QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 DB 317 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 376
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
 DB 377 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 436
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
 DB 437 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 466

RESULT 11
 Q6N089 HUMAN
 ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
 AC Q6N089;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686f15220.
 GN Name=DKFZp686f15220;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Rectum tumor;
 RG The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the ENBL/GenBank/DBJ databases.
 DR EMBL; BX640627; CAE45781.1; -, mRNA.
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 472;
 Best Local Similarity 97.6%; Pred. No. 1.6e-118;
 Matches 322; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 DB 143 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 202
 QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELGG 120
 DB 203 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELGG 262
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 DB 263 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 322
 QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 DB 323 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 382
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
 DB 383 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 442
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
 DB 443 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 472

RESULT 12
 Q6P055 HUMAN
 ID Q6P055 HUMAN PRELIMINARY; PRT; 473 AA.
 AC Q6P055;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RE EMBL; BC065820; AAH65820.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 473;
Best Local Similarity 97.6%; Pred. No. 1.9e-118;
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203

QY 61 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPCPAPPELLGG 120
DB 204 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPCPAPPELLGG 263

QY 121 PSVFLPPPKPDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 264 PSVFLPPPKPDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 323

QY 181 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 324 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 383

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 384 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 443

QY 301 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 330
DB 444 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 473

RESULT 13
Q6MZQ6 HUMAN
ID Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RE EMBL; BX640947; CAE45972.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6MZQ6; 20-475.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 475;
Best Local Similarity 97.6%; Pred. No. 1.9e-118;
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 205

QY 61 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPCPAPPELLGG 120
DB 206 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPCPAPPELLGG 265

QY 121 PSVFLPPPKPDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 266 PSVFLPPPKPDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 325

QY 181 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 326 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 385

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 445

QY 301 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 330
DB 446 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 475

RESULT 14
Q6N094 HUMAN
ID Q6N094_HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O01196.
GN Name=DKFZp686O01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RE EMBL; BX640622; CAE45776.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 480;
 Best Local Similarity 97.6%; Pred. No. 1.9e-118;
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 151 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 210
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCCPCPAPELLGG 120
 DB 211 GLYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCCPCPAPELLGG 270
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
 DB 271 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 330
 QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
 DB 331 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 390
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 300
 DB 391 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 450
 QY 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330
 DB 451 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 480

RESULT 15
 Q6N097_HUMAN
 ID Q6N097_HUMAN PRELIMINARY; PRT; 481 AA.
 AC Q6N097;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686H20196.
 GN Name=DKFZp686H20196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Esophagus tumor;
 RG The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Pobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640619; CA645773.1; -; mRNA.
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 481;
 Best Local Similarity 97.6%; Pred. No. 1.9e-118;
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 152 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 211
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCCPCPAPELLGG 120
 DB 212 GLYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCCPCPAPELLGG 271
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
 DB 272 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 331
 QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
 DB 332 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 391
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 300
 DB 392 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 451
 QY 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330
 DB 452 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 481

Search completed: February 22, 2006, 21:37:12
 Job time : 222.43 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 22, 2006, 21:57:24 ; Search time 168.705 Seconds
(without alignments)
817.308 Million cell updates/sec
Title: US-10-000-439-2
Perfect score: 1764
Sequence: 1 ASTKGPSVFPPLAPSSKSTSG.....MHEALHNHYQQRSLSPGK 330
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap:*
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1764	100.0	330	3	US-09-847-208-2
2	1764	100.0	330	4	US-10-000-439-2
3	1732	98.2	330	5	US-10-966-673-29
4	1729	98.0	330	3	US-09-995-898A-15
5	1729	98.0	330	3	US-09-892-949-38
6	1729	98.0	330	4	US-10-047-542-20
7	1729	98.0	330	4	US-10-269-805-68
8	1729	98.0	330	4	US-10-310-719-8
9	1729	98.0	330	4	US-10-112-582-1
10	1729	98.0	330	4	US-10-320-231A-81
11	1729	98.0	330	4	US-10-383-902A-6
12	1729	98.0	330	4	US-10-408-901-2
13	1729	98.0	330	4	US-10-420-034A-15
14	1729	98.0	330	4	US-10-257-907-5
15	1729	98.0	330	4	US-10-656-769-2
16	1729	98.0	330	4	US-10-772-531-38
17	1729	98.0	330	4	US-10-479-326-1
18	1729	98.0	330	5	US-10-815-449-8
19	1729	98.0	330	5	US-10-684-957-2
20	1729	98.0	330	5	US-10-886-838-6
21	1729	98.0	330	5	US-10-822-300-3
22	1729	98.0	330	5	US-10-822-300-7
23	1729	98.0	330	5	US-10-687-118-3
24	1729	98.0	330	5	US-10-687-118-7
25	1729	98.0	330	5	US-10-901-735-2
26	1729	98.0	330	5	US-10-698-907-22
27	1729	98.0	330	5	US-10-928-305-7

28	1729	98.0	330	5	US-10-480-109-5	Sequence 5, Appli
29	1729	98.0	330	5	US-10-891-658-2	Sequence 2, Appli
30	1729	98.0	330	5	US-10-867-506-81	Sequence 81, Appl
31	1729	98.0	330	5	US-10-937-596-31	Sequence 31, Appl
32	1729	98.0	330	5	US-10-893-576-45	Sequence 45, Appl
33	1729	98.0	330	5	US-10-868-373-8	Sequence 8, Appli
34	1729	98.0	330	5	US-10-977-369-139	Sequence 139, App
35	1729	98.0	330	5	US-10-901-736-60	Sequence 60, Appl
36	1729	98.0	330	5	US-10-982-555-38	Sequence 38, Appl
37	1729	98.0	330	6	US-11-004-054-1	Sequence 1, Appli
38	1729	98.0	330	6	US-11-026-998-22	Sequence 22, Appl
39	1729	98.0	330	6	US-11-027-309A-22	Sequence 22, Appl
40	1729	98.0	330	6	US-11-090-836-44	Sequence 44, Appl
41	1729	98.0	330	6	US-11-090-846-44	Sequence 44, Appl
42	1729	98.0	330	6	US-11-090-847-44	Sequence 44, Appl
43	1729	98.0	330	6	US-11-102-403-24	Sequence 24, Appl
44	1729	98.0	332	3	US-09-990-586-98	Sequence 98, Appl
45	1729	98.0	332	4	US-10-310-113-167	Sequence 167, App

ALIGNMENTS

RESULT 1
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67 002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match	100.0%	Score 1764;	DB 3;	Length 330;
Best Local Similarity	100.0%	Pred. No. 1.3e-128;		
Matches 330;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS	60	
Db	1	ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS	60	
Qy	61	GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG	120	
Db	61	GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG	120	
Qy	121	PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQYN	180	
Db	121	PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQYN	180	
Qy	181	STYRVSVVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE	240	
Db	181	STYRVSVVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE	240	
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDVGSFFLYSLKLTVDKSKW	300	
Db	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDVGSFFLYSLKLTVDKSKW	300	
Qy	301	QCGNVFSCSVMEALHNNHYQQRSLSPGK 330		
Db	301	QCGNVFSCSVMEALHNNHYQQRSLSPGK 330		

RESULT 2

US-10-000-439-2
 ; Sequence 2, Application US/10000439
 ; Publication No. US20030064063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saxon, Andrew
 ; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
 ; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
 ; FILE REFERENCE: U067.004A
 ; CURRENT APPLICATION NUMBER: US/10/000.439
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: US 09/847,208
 ; PRIOR FILING DATE: 2001-05-01
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-000-439-2

Query Match 100.0%; Score 1764; DB 4; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
 Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
 Qy 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Qy 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Db 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSGFFFLYSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSGFFFLYSKLTVDKSRW 300
 Qy 301 QQGNVFSCSVNHEALHNHYQORSLSPGK 330
 Db 301 QQGNVFSCSVNHEALHNHYQORSLSPGK 330

RESULT 3

US-10-966-673-29
 ; Sequence 29, Application US/10966673
 ; Publication No. US20050226864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Protein Design Labs, Inc.
 ; APPLICANT: Hinton, Paul R
 ; APPLICANT: Tsurushita, Naoya
 ; TITLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
 ; FILE REFERENCE: 05882.0039.NPUS07
 ; CURRENT APPLICATION NUMBER: US/10/966.673
 ; CURRENT FILING DATE: 2004-10-15
 ; PRIOR APPLICATION NUMBER: US 60/562,627
 ; PRIOR FILING DATE: 2004-04-14
 ; PRIOR APPLICATION NUMBER: US 60/511,687
 ; PRIOR FILING DATE: 2003-10-15
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 29
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-10-966-673-29

Query Match 98.2%; Score 1732; DB 5; Length 330;
 Best Local Similarity 98.2%; Pred. No. 4e-126; 4; Indels 0; Gaps 0;
 Matches 324; Conservative 2; Mismatches 2;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
 Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
 Qy 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Qy 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Db 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSGFFFLYSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSGFFFLYSKLTVDKSRW 300
 Qy 301 QQGNVFSCSVNHEALHNHYQORSLSPGK 330
 Db 301 QQGNVFSCSVNHEALHNHYQORSLSPGK 330

RESULT 4

US-09-995-898A-15
 ; Sequence 15, Application US/09995898A
 ; Publication No. US20030027253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Xu, Wenfeng
 ; APPLICANT: No. US20030027253Alak, Julia E.
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Grant, Francis J.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
 ; FILE REFERENCE: 00-108
 ; CURRENT APPLICATION NUMBER: US/09/995,898A
 ; CURRENT FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/253,561
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/267,211
 ; PRIOR FILING DATE: 2001-02-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-995-898A-15

Query Match 98.0%; Score 1729; DB 3; Length 330;
 Best Local Similarity 97.9%; Pred. No. 6.8e-126; 4; Indels 0; Gaps 0;
 Matches 323; Conservative 3; Mismatches 4;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
 Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
 Qy 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Qy 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
QY 301 QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330

RESULT 5
US-09-892-949-38
; Sequence 38, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-38

Query Match 98.0%; Score 1729; DB 3; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 120
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
QY 301 QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330

RESULT 6
US-10-047-542-20
; Sequence 20, Application US/10047542

; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-20

Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 120
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
QY 301 QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330

RESULT 7
US-10-269-805-68
; Sequence 68, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-68

Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVHNKTKPREQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVHNKTKPREQYN 180
QY 181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
DB 181 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLLYSLKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 8

US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: IgG1 constant region

US-10-310-719-8

Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVHNKTKPREQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVHNKTKPREQYN 180
QY 181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
DB 181 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLLYSLKLTVDKSRW 300

DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLLYSLKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 9

US-10-112-582-1
; Sequence 1, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: human Ig gamma heavy chain C region

US-10-112-582-1

Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVHNKTKPREQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVHNKTKPREQYN 180
QY 181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
DB 181 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLLYSLKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 10

US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19

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; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-231A-81

Query Match          98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

QY 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 11
US-10-383-902A-6
; Sequence 6, Application US/10383902A
; Publication No. US20030224408A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Mullberg, Jurgen
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
; FILE REFERENCE: 10280-042001
; CURRENT APPLICATION NUMBER: US/10/383,902A
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/362,403
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated plasmid sequence
US-10-383-902A-6

Query Match          98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

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DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120
QY 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 12
US-10-408-901-2
; Sequence 2, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-2

Query Match          98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120
QY 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 13

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US-10-420-034A-15
; Sequence 15, Application US/10420034A
; Publication No. US20040029228A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20040029228A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Klucher, Kevin M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; CURRENT APPLICATION NUMBER: US/10/420,034A
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,813
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-420-034A-15

Query Match      98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPPETVTVSNWNGALTSVHTTTPAVLQSS 60

Qy 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120
Db 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 14
US-10-257-907-5
; Sequence 5, Application US/10257907
; Publication No. US20040043022A1
; GENERAL INFORMATION:
; APPLICANT: Heuer, Josef
; APPLICANT: Liu, Jingqi
; APPLICANT: Na, Songqing
; APPLICANT: Song, Ho Yeong
; APPLICANT: Yang, Derek Di
; TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
; FILE REFERENCE: X-13992
; CURRENT APPLICATION NUMBER: US/10/257,907
; CURRENT FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-907-5

Query Match      98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPPETVTVSNWNGALTSVHTTTPAVLQSS 60

Qy 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120
Db 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
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; ORGANISM: Homo sapiens
US-10-257-907-5

Query Match      98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPPETVTVSNWNGALTSVHTTTPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPPETVTVSNWNGALTSVHTTTPAVLQSS 60

Qy 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120
Db 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 15
US-10-656-769-2
; Sequence 2, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01.1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-2

Query Match      98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPPETVTVSNWNGALTSVHTTTPAVLQSS 60

Qy 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120
Db 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPAPPELLGG 120

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
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Qy	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330
Db	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330

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Job time : 170.705 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:58:19 ; Search time 17.0984 Seconds
(without alignments)
287.324 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*

- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1729	98.0	330	6	US-10-886-383-6
2	1729	98.0	330	6	US-10-493-909-20
3	1729	98.0	330	6	US-10-982-440-68
4	1729	98.0	330	7	US-11-022-289-11
5	1729	98.0	330	7	US-11-075-351-1
6	1729	98.0	330	7	US-11-165-141-15
7	1729	98.0	330	7	US-11-102-621-3
8	1729	98.0	330	7	US-11-102-621-7
9	1729	98.0	330	7	US-11-005-726-164
10	1729	98.0	330	7	US-11-124-620-1
11	1729	98.0	330	7	US-11-233-683-1
12	1729	98.0	335	7	US-11-024-251-35
13	1729	98.0	444	7	US-11-172-320-6
14	1729	98.0	444	7	US-11-173-969-6
15	1729	98.0	450	7	US-11-005-726-161
16	1729	98.0	450	7	US-11-049-536-701
17	1729	98.0	451	7	US-11-158-505-33
18	1729	98.0	470	7	US-11-072-512-3730
19	1729	98.0	551	7	US-11-022-289-7
20	1729	98.0	551	7	US-11-022-289-8
21	1729	98.0	557	7	US-11-022-289-4
22	1729	98.0	557	7	US-11-022-289-5
23	1729	98.0	557	7	US-11-022-289-6
24	1727	97.9	592	6	US-10-016-686-4
25	1726	97.8	330	7	US-11-102-621-71

ALIGNMENTS

RESULT 1

US-10-886-383-6

; Sequence 6, Application US/10886383

; Publication No. US20060005571A1

; GENERAL INFORMATION:

; APPLICANT: Hoffmann-La Roche Inc.

; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and use

; TITLE OF INVENTION: thereof

; FILE REFERENCE: 21695

; CURRENT APPLICATION NUMBER: US/10/886,383

; CURRENT FILING DATE: 2004-07-08

; PRIOR APPLICATION NUMBER: EP 03015526

; PRIOR FILING DATE: 2003-07-10

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 330

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-886-383-6

Query Match

Best Local Similarity 98.0%; Score 1729; DB 6; Length 330;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60

Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120

Db 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120

QY 121 PSVFLPPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 180

Db 121 PSVFLPPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 180

QY 181 STYRVSVLVTLVHQNMMGKEYCKVSKNKPAPTEKTSKAKVOPREQVVTLPSPRDE 240

Db 181 STYRVSVLVTLVHQNMMGKEYCKVSKNKPAPTEKTSKAKVOPREQVVTLPSPRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVGSFFLYSKLTVDKSRW 300

Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVGSFFLYSKLTVDKSRW 300

QY 301 QGQNVFSCSVMEALHNHYQORSLSLSPGK 330

Db 301 QGQNVFSCSVMEALHNHYQORSLSLSPGK 330

Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNNHYQORSLSPGK 330
Db 301 QQGNVFSCSVMEALHNNHYTKQSLSPGK 330

RESULT 5

US-11-075-351-1
; Sequence 1, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-1

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHHTCPPCPAPPELLGG 120
Db 61 GLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHHTCPPCPAPPELLGG 120
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHONNMNCKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHONNMNCKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNNHYQORSLSPGK 330
Db 301 QQGNVFSCSVMEALHNNHYTKQSLSPGK 330

RESULT 6

US-11-165-141-15
; Sequence 15, Application US/11165141
; Publication No. US2005026485A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Novak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/11/165,141
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/09/995,898
; PRIOR FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-165-141-15

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHHTCPPCPAPPELLGG 120
Db 61 GLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHHTCPPCPAPPELLGG 120
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHONNMNCKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHONNMNCKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNNHYQORSLSPGK 330
Db 301 QQGNVFSCSVMEALHNNHYTKQSLSPGK 330

RESULT 7

US-11-102-621-3
; Sequence 3, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-3

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
RESULT 8
US-11-102-621-7
; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: ANTIBODIES BY MUTAGENESIS
; CURRENT FILING DATE: 2005-04-08
; PRIOR FILING DATE: 2005-04-08
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-11-102-621-7

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
RESULT 9
US-11-005-726-164
; Sequence 164, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDORF, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566
; PRIOR FILING DATE: 2002-11-11
; PRIOR APPLICATION NUMBER: EP 01126858.8
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain
; OTHER INFORMATION: constant region
US-11-005-726-164

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330

RESULT 10
US-11-124-620-1
; Sequence 1, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur

APPLICANT: Vafa, Omid
APPLICANT: Hayes, Robert
TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71386-9
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: US 60/568,440
PRIOR FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/589,906
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/627,026
PRIOR FILING DATE: 2004-11-09
PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/627,774
PRIOR FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US 10/822,231
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US 10/379,392
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-11-124-620-1

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKALPKVKKPKSCDKTHHTCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKALPKVKKPKSCDKTHHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QGQNVFSCSVMEALHNNHYQORSLSPGK 330
DB 301 QGQNVFSCSVMEALHNNHYQORSLSPGK 330

RESULT 11
US-11-233-683-1
Sequence 1, Application US/11233683
Publication No. US20060025573A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
FILE REFERENCE: LEX-017
CURRENT APPLICATION NUMBER: US/11/233,683
CURRENT FILING DATE: 2005-09-23
PRIOR APPLICATION NUMBER: US 60/280,625
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.0

SEQ ID NO 1
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: human Ig gamma heavy chain C region
US-11-233-683-1
Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKALPKVKKPKSCDKTHHTCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKALPKVKKPKSCDKTHHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QGQNVFSCSVMEALHNNHYQORSLSPGK 330
DB 301 QGQNVFSCSVMEALHNNHYQORSLSPGK 330
RESULT 12
US-11-024-251-35
Sequence 35, Application US/11024251
Publication No. US20050266425A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
FILE REFERENCE: 1843.0230001
CURRENT APPLICATION NUMBER: US/11/024,251
CURRENT FILING DATE: 2004-12-29
PRIOR APPLICATION NUMBER: 60/533,241
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35
LENGTH: 335
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: IGG Secreted Constant Domain
US-11-024-251-35
Query Match 98.0%; Score 1729; DB 7; Length 335;
Best Local Similarity 97.9%; Pred. No. 2.9e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 60
DB 6 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVQLSS 65
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKALPKVKKPKSCDKTHHTCPCPAPPELLGG 120
DB 66 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKALPKVKKPKSCDKTHHTCPCPAPPELLGG 125

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Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
Db 126 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 185
Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 240
Db 186 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 245
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFPLYSKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFPLYSKLTVDKSRW 305
Qy 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 306 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 335

RESULT 13
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6
Query Match 98.0%; Score 1729; DB 7; Length 444;
Best Local Similarity 97.9%; Pred. No. 4e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLPAPSSKSTSGGTAALGLCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 115 ASTKGPSVFLPAPSSKSTSGGTAALGLCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 174
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 120
Db 175 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 234
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
Db 235 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 294
Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 240
Db 295 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 354
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFPLYSKLTVDKSRW 300
Db 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFPLYSKLTVDKSRW 414
Qy 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 306 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 335

RESULT 15
US-11-005-726-161
; Sequence 161, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566
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Db 415 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 444

RESULT 14
US-11-173-969-6
; Sequence 6, Application US/11173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-11-173-969-6
Query Match 98.0%; Score 1729; DB 7; Length 444;
Best Local Similarity 97.9%; Pred. No. 4e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLPAPSSKSTSGGTAALGLCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 115 ASTKGPSVFLPAPSSKSTSGGTAALGLCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 174
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 120
Db 175 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 234
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
Db 235 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 294
Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 240
Db 295 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPOVYTLPPSRDE 354
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFPLYSKLTVDKSRW 300
Db 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFPLYSKLTVDKSRW 414
Qy 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 415 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 444

RESULT 15
US-11-005-726-161
; Sequence 161, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566
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; PRIOR FILING DATE: 2002-11-11
; PRIOR APPLICATION NUMBER: EP 01126858.8
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain
US-11-005-726-161

Query Match	98.0%;	Score 1729;	DB 7;	Length 450;
Best Local Similarity	97.9%;	Pred. No. 4.1e-132;		
Matches 323;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	1	ASTKGSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS	60
Db	121	ASTKGSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS	180
Qy	61	GLYSLSVVTVPSSSLGTTIYICNVNHPKNTKVDKKVPEPKSCDKTHTCPPCPAPPELLGG	120
Db	181	GLYSLSVVTVPSSSLGTTIYICNVNHPKNTKVDKKVPEPKSCDKTHTCPPCPAPPELLGG	240
Qy	121	PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN	180
Db	241	PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN	300
Qy	181	STYRVVSVLTVHLQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE	240
Db	301	STYRVVSVLTVHLQNMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE	360
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	300
Db	361	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	420
Qy	301	QQGNVFSCSVMHEALHNHYQQRSLSPGK	330
Db	421	QQGNVFSCSVMHEALHNHYQQRSLSPGK	450

Search completed: February 22, 2006, 22:03:44
Job time : 19.0984 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:31:15 ; Search time 23.6408 Seconds
(without alignments)
944.229 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNYQQRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	370	1 GHU	Ig gamma-1 chain C
2	1219	96.7	334	2 S69339	Ig heavy chain V r
3	1217	96.6	255	4 S31866	Ig gamma-1 chain C
4	1172	93.0	234	2 PT0207	Ig gamma-3 chain C r
5	1138	90.3	377	2 A23511	Ig gamma-3 chain C
6	1136	90.2	377	2 A60764	Ig gamma-3 heavy C
7	1123	89.1	289	1 G3HUI	Ig gamma-2 chain C
8	1107	87.9	326	1 G2HU	Ig gamma-4 chain C
9	1097	87.1	327	1 G4HU	Ig gamma-4 chain C r
10	883	70.1	323	1 GHRB	Ig gamma-2 chain C
11	868.5	68.9	328	2 I47160	Ig gamma-2 chain C
12	868.5	68.9	328	2 I47159	Ig gamma-2a chain
13	865	68.7	277	2 I47162	Ig gamma-4 chain C
14	858	68.1	329	1 G2GP	Ig gamma-2 chain C
15	847.5	67.3	328	2 I47158	Ig gamma-1 chain c
16	840.5	66.7	328	2 I47161	Ig gamma-3 chain c
17	820	65.1	470	2 S22080	Ig heavy chain pre
18	813	64.5	333	3 PS0018	Ig gamma-2b chain C
19	812.5	64.5	329	2 G3MSC	Ig gamma-3 chain C
20	811.5	64.4	308	2 C30554	Ig heavy chain C r
21	811.5	64.4	472	2 S31459	Ig gamma-1 chain -
22	801.5	63.6	398	1 G3MSM	Ig gamma-3 chain C
23	794.5	63.1	444	2 PC4436	monoclonal antibod
24	789.5	62.7	324	1 G1MS	Ig gamma-1 chain C
25	784.5	62.3	393	1 PS0017	Ig gamma-1 chain C
26	784.5	62.3	393	1 G1MSM	Ig gamma-1 chain C
27	776.5	61.6	329	2 S00847	Ig gamma-2c chain
28	776	61.6	330	1 G2MSA	Ig gamma-2a chain
29	776	61.6	469	2 S37483	Ig gamma-2a chain

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034COE; EMBL:Z17370

A>Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,

A>Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequer

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, 'R', 98-135 <CUN>

A:Cross-references: UNIPARC:UPI000017378D

A>Note: This sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,

A:Cross-references: UNIPARC:UPI000017378E

A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2b chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma heavy cha
Ig gamma heavy cha
Ig heavy chain VHI
Ig heavy chain V-I
Ig gamma-1 chain C
Ig Y heavy chain (C
Ig heavy chain pre
Ig mu chain C regi
Ig mu chain C regi

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), Igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Cross-references: UNIPARC:UPI000017378F
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KO1
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KO1; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Cross-references: UNIPARC:UPI0000173790
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: Interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: Interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 97.28; Score 1225; DB 1; Length 330;
Best Local Similarity 97.08; Pred. No. 1.7e-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSPGK 232
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSPGK 330
RESULT 2
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
Query Match 96.7%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 5.5e-85;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 143 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 203 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 262
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 263 ISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 322
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSPGK 232
Db 323 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSPGK 374
RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filipula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PI
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
Query Match 96.6%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 4.9e-85;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 24 ESKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 84 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 143

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QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 144 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTTTP 203
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
|||||
Db 204 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 255
|||||

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991.
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
A:Cross-references: UNIPARC:UPI0000176F05
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 1172; DB 2; Length 234;
Best Local Similarity 95.6%; Pred. No. 1.1e-81;
Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
Db 10 EPKSCDTTHTCPCAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 69
|||||
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKT 120
|||||
Db 70 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKT 129
|||||
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 130 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTTTP 189
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQS 225
|||||
Db 190 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQKS 234
|||||

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA
A:Reference number: A23511, MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272
C:Genetics:
A:Gene: IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 1138; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 7.5e-79;
```

```
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
Db 146 EPKSCDTTTPPCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVQF 205
|||||
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKT 120
|||||
Db 206 KMYVDGVEVHNKTKPREEQYNSTFRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKT 265
|||||
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 266 ISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPSDIAVWESSGQPENNYNTTP 325
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
|||||
Db 326 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNRFQKSLSLSPGK 377
|||||

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conversion
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:O8N4V9; UNIPARC:UPI0000176F0B
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 1136; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 1.1e-78;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
Db 146 EPKSCDTTTPPCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVQF 205
|||||
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKT 120
|||||
Db 206 KMYVDGVEVHNKTKPREEQYNSTFRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKT 265
|||||
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 266 ISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPSDIAVWESSGQPENNYNTTP 325
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
|||||
Db 326 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNRFQKSLSLSPGK 377
|||||

RESULT 7
G3HUW1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein
A:Reference number: A90442; MUID:81021548; PMID:6774747
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
```

A:Cross-references: UNIPARC:UPI0000173797
A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A:Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A:Reference number: A92219; MUID:77118561; PMID:402363
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein w
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A:Cross-references: UNIPARC:UPI0000173798
A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A:Cross-references: UNIPARC:UPI0000173799
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R:Alexander, A.; Steinmetz, M.; Barricault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70;72-114;116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A:Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C;
A:Note: a carboxyl-terminal Lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domain: immunoglobulin homology <IM3>
F:1/Modified site: pyroglutamic acid (Gln) #status experimental
F:6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 89.1%; Score 1123; DB 1; Length 289;
Best Local Similarity 88.3%; Pred. No. 7.5e-78;
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy	1	EPKSDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Db	59	EPKSCDTPPCPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF	118
Qy	61	NWYVDGVEHNKVKPREEQNSYRVVSVLTVLHQWMMGKEYCKVKSNKALPAPIEKT	120
Db	119	KWYVDGVQVHNKVKPREEQNSYRVVSVLTVLHQWLDGKEYCKVKSNKALPAPIEKT	178
Qy	121	ISKAKVPRPQVVTLPSPRDELTKQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTP	180
Db	179	ISKTKGQPREPQVVTLPSPREMTKNQVSLTCLVKGPYPSDIAVEWESSQPENNYNTTP	238
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFNCSVMHEALHNNHQQRSLSLSPG	231
Db	239	PMLDSGGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNNFTQKLSLSLSPG	289

RESULT 8
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:93;
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein TII
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Cross-references: UNIPARC:UPI0000173791
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation: myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM3>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.9%; Score 1107; DB 1; Length 326;

Best Local Similarity 88.4%; Pred. No. 1.4e-76;
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 ERKCCVE---CPCPAPP--VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 154

QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT 120
DB 155 NMYVDGVEVHNKTKPREEQFNSTFRVSVLTIVVHQDLNGKEYKCKVSNKGLPAPIEKT 214

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
DB 215 ISKTKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 274

QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNFVSCVMHEALHNNHYQOORSLSPGK 232
DB 275 PMLDSGSEFPLYSKLTVDKSRWQQGNFVSCVMHEALHNNHYQOORSLSPGK 326

RESULT 9
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299862
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A>Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30; 81-326 <PIN>
A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.1%; Score 1097; DB 1; Length 327;
Best Local Similarity 90.5%; Pred. No. 8.1e-76;
Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 11 CPCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 70
DB 106 CPSCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 165

QY 71 NVKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
DB 166 NAKTKPREEQFNSTYRVSVLTVLHQNMMNGKEYKCKVSNKGLPFLSIEKTISKAKVQPRE 225

QY 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSVGSFF 190
DB 236 PQVYTLPPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSVGSFF 285

QY 191 LYSKLTVDKSRWQQGNFVSCVMHEALHNNHYQOORSLSPGK 232
DB 286 LYSRLTVDKSRWQEGNFGVSCVMHEALHNNHYQOORSLSPGK 327

RESULT 10
CHRB
Ig gamma chain C region - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text_change 09-Jul-2004
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplo.
A:Reference number: A91749; MUID:84030930; PMID:6313520
A:Accession: A91749
A:Molecule type: mRNA
A:Residues: 1-323 <BER>
A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A>Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Th.
R:Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A:Reference number: A90290; MUID:76135469; PMID:1243651
A:Accession: A90290
A:Molecule type: protein
A:Residues: 1-47, 'B', 49-71, 'PV', 72-128 <PRA>
A:Cross-references: UNIPARC:UPI00001737AB
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A:Reference number: A93928; MUID:83299917; PMID:6193512
A:Accession: A93928
A:Molecule type: mRNA
A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A:Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:G165111; PIDN:AAA31289.1; PID
A>Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic mark.
R:Richter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
A:Reference number: A90245; MUID:70110015; PMID:5461106
A:Accession: A90245
A:Molecule type: protein
A:Residues: 132-143, 'E', 145-161 <FRU>
A:Cross-references: UNIPARC:UPI00001737AC
R:Hall, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A:Reference number: A94416
A:Accession: A94416
A:Molecule type: protein
A:Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',
A:Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE
A>Note: this has the e15 allotypic marker, 185-Ala
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.1%; Score 883; DB 1; Length 323;
Best Local Similarity 64.5%; Pred. No. 1.3e-59;
Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 44
DB 76 PQVTCNVAHPATNTKVTAPSTCSTKPTCPPELLGGPSVFLFPPKPKDTLMISRTPEV 135

Qy 45 TCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYNSTYRVVSVLTVLHQWNMNGKEY 104
Db 136 TCVVVDVSDDEPEVKFNWYVDGVEVHNKTKPRREQYNSTYRVVSVLTVLHQWNMNGKEY 195
Qy 105 KCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 164
Db 196 KCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 255
Qy 165 EWESNGQPENNYTKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQOR 224
Db 256 EWEKNGKAEDNYKTTPPAVLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQOR 315
Qy 225 SLSLSPGK 232
Db 316 SISRSPGK 323

RESULT 11

I47160
Ig gamma 2b chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47160
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47160
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:G433125; PIDN:AAA52218.1; P
C/Genetics:
C/Superspecies: immunoglobulin C region; immunoglobulin homology <IMM>
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 1.6e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;
Qy 11 CPPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
Db 106 CPICPACE-SPGSVFIFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164
Qy 71 NVKTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKKVSNNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKEEQYNSTYRVVSVLTVLHQWNMNGKEYCKKVSNNKALPAPIEKTISKAKVQPRE 224
Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPPVLDSVGS 188
Db 225 PQVYTLPPHABELSRKSVITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPQQDVGDT 284
Qy 189 FFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSPGK 232
Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNNHYTKSISKTGK 328

RESULT 12

I47159
Ig gamma 2a chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47159
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47159
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>

A/Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:G433123; PIDN:AAA52217.1; P
C/Genetics:
A/Gene: IgG2a
C/Superspecies: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 1.6e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Qy 11 CPPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
Db 106 CPICPACE-SPGSVFIFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164
Qy 71 NVKTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKKVSNNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKEEQYNSTYRVVSVLTVLHQWNMNGKEYCKKVSNNKALPAPIEKTISKAKVQPRE 224
Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPPVLDSVGS 188
Db 225 PQVYTLPPHABELSRKSVITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPQQDVGDT 284
Qy 189 FFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSPGK 232
Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNNHYTKSISKTGK 328

RESULT 13

I47162
Ig gamma 4 chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47162
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47162
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-277 <KAC>
A/Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:G433129; PIDN:AAA52220.1; P
C/Genetics:
C/Superspecies: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 865; DB 2; Length 277;
Best Local Similarity 69.0%; Pred. No. 2.5e-58;
Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;
Qy 8 THTCPDPCP-APELLG-GPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65
Db 49 TKTTPCPICPACGEGPGSAFIFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 108
Qy 66 GVEVHNKTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKKVSNNKALPAPIEKTISKAK 125
Db 109 GVEVHTAQTAPKEEQYNSTYRVVSVLTVLHQWNMNGKEYCKKVSNNKALPAPIEKTISKAK 168
Qy 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPPVL 183
Db 169 GQTRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPPVL 228
Qy 184 DSVGSFLLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSPGK 232
Db 229 DVDGTLYFLYSKLAVDKASWQGGDTFOCAVMHEALHNNHYTKSIFKTPGK 277

RESULT 14

G2GP
Ig gamma-2 chain C region - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004

C:Accession: A94553; A90352; A90359; A90384; A90385; A02151
R:Trischmann, T.M.
submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553
A:Molecule type: protein
A:Residues: 1-3 <TRI>
A:Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E
R:Birshtein, B.K.; Hussein, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
Biochemistry 10, 18-25, 1971
A:Reference number: A90352; MUID:71058471; PMID:5538606
A:Accession: A90352
A:Molecule type: protein
A:Residues: 4-68 <BIR>
A:Cross-references: UNIPARC:UPI000017379F
R:Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
Biochemistry 10, 9-17, 1971
A:Reference number: A90359; MUID:71058486; PMID:5538616
A:Accession: A90359
A:Molecule type: protein
A:Residues: 69-133;312-329 <TUR>
A:Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072; PMID:4429665
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
A:Cross-references: UNIPARC:UPI00001737A2
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073; PMID:4609467
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
A:Cross-references: UNIPARC:UPI00001737A3
R:Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474; PMID:4922544
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 1e-57;
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

QY 1 EPKSCDKTTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 101 ZPBPCC---TCPCPPPELGGPSVFIFFPKPKDTLMISLTPTVTCVVVDVSDPEVQF 156
QY 61 NMYVDGVEVHNKTPREQYNSTYRVSVLTVLHQNMMNGKCYKCKVSNKALPAPIEKT 120
DB 157 TWFVDNKPVGNAETKPRVEQYNTTFRVESVLPFIHQDNLRGKFKCKVYNKALPAPIEKT 216
QY 121 ISKAKVQRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT 178

DB 217 ISKTKGAPRPDVTYTLPPSRDELTKNQVSLTCLINFFPADIHVWASNRVPSKEYKN 276
QY 179 TTPVLDSDVSGRPFLYSKLTVDKSRWQGNVFCSSVMHEALHNHYQQRSLSPG 231
DB 277 TPPIEDADGSGFLYSKLTVDKSAWDQGTYYTCSVMHEALHNHYTKAIRSPG 329

RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47158
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:G4333121; PIDN:AAA52216.1; P
C:Genetics:
A:Gene: IgG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 847.5; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 6.4e-57;
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

QY 10 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 69
DB 105 TCPICPGCE-VAGPSVFIFFPKPKDTLMISQTPETVCVVVDVSKHAQVQFSWYVDGVEV 163
QY 70 HNVKTKPREQYNSTYRVSVLTVLHQNMMNGKCYKCKVSNKALPAPIEKTISKAKVQPR 129
DB 164 HTAETRPKEQFNSTYRVSVVLPFIHQDNLGKFKCKVNNVDLPAPITRTTISKATGQSR 223
QY 130 EQQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDSDVG 187
DB 224 EQVYTLPPPAEELSRSKVTTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTTPPQQDVG 283
QY 188 SFFLYSKLTVDKSRWQGNVFCSSVMHEALHNHYQQRSLSPG 232
DB 284 TFFLYSLKLVKARWDHGDGKFECAVMHEALHNHYTKSISKTQK 328

Search completed: February 22, 2006, 21:38:17
Job time : 24.6408 secs

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:37:34 ; Search time 34.4594 Seconds
(without alignments)
556.619 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCCPPAPPELL.....MHEALHNYQORSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep:*
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- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	232	1 US-08-595-043A-50	Sequence 50, Appl
2	1225	97.2	232	2 US-09-968-362A-26	Sequence 26, Appl
3	1225	97.2	232	2 US-09-932-812A-26	Sequence 26, Appl
4	1225	97.2	331	2 US-09-178-869-2	Sequence 2, Appl
5	1225	97.2	331	2 US-09-761-413-2	Sequence 2, Appl
6	1225	97.2	360	2 US-09-180-100-11	Sequence 11, Appl
7	1225	97.2	360	2 US-09-949-713-11	Sequence 11, Appl
8	1225	97.2	371	1 US-08-236-311-7	Sequence 7, Appl
9	1225	97.2	371	2 US-08-457-918-7	Sequence 7, Appl
10	1225	97.2	371	2 US-10-157-408-7	Sequence 7, Appl
11	1225	97.2	376	2 US-09-180-100-22	Sequence 22, Appl
12	1225	97.2	376	2 US-09-949-713-22	Sequence 22, Appl
13	1225	97.2	379	2 US-10-679-993-9	Sequence 9, Appl
14	1225	97.2	396	1 US-08-784-512-3	Sequence 3, Appl
15	1225	97.2	396	2 US-09-176-228-3	Sequence 3, Appl
16	1225	97.2	424	4 PCT-US95-03866-12	Sequence 12, Appl
17	1225	97.2	424	4 PCT-US95-03866-14	Sequence 14, Appl
18	1225	97.2	437	4 PCT-US96-10043-11	Sequence 11, Appl
19	1225	97.2	442	4 PCT-US96-10043-9	Sequence 9, Appl
20	1225	97.2	442	4 PCT-US96-10043-7	Sequence 7, Appl
21	1225	97.2	446	1 US-08-397-411-7	Sequence 13, Appl
22	1225	97.2	449	1 US-08-458-516-13	Sequence 16, Appl
23	1225	97.2	452	2 US-09-773-877B-16	Sequence 7, Appl
24	1225	97.2	459	1 US-08-157-101A-7	Sequence 18, Appl
25	1225	97.2	462	2 US-09-773-877B-18	Sequence 41, Appl
26	1225	97.2	467	2 US-08-030-175-41	Sequence 42, Appl
27	1225	97.2	467	2 US-08-030-175-42	Sequence 42, Appl

28	1225	97.2	470	2 US-10-104-047-3730	Sequence 3730, Ap
29	1225	97.2	475	2 US-09-740-002-27	Sequence 27, Appl
30	1225	97.2	476	1 US-08-378-939-10	Sequence 10, Appl
31	1225	97.2	476	2 US-08-487-550-4	Sequence 4, Appl
32	1225	97.2	476	2 US-08-487-550-12	Sequence 12, Appl
33	1225	97.2	476	2 US-09-526-098-4	Sequence 4, Appl
34	1225	97.2	476	2 US-09-526-098-12	Sequence 12, Appl
35	1225	97.2	476	2 US-09-383-916-4	Sequence 4, Appl
36	1225	97.2	476	2 US-09-383-916-12	Sequence 12, Appl
37	1225	97.2	476	2 US-09-758-173-4	Sequence 4, Appl
38	1225	97.2	476	2 US-09-758-173-12	Sequence 12, Appl
39	1225	97.2	476	2 US-09-576-424-4	Sequence 4, Appl
40	1225	97.2	476	2 US-09-576-424-12	Sequence 12, Appl
41	1225	97.2	478	2 US-08-487-550-8	Sequence 8, Appl
42	1225	97.2	478	2 US-09-526-098-8	Sequence 8, Appl
43	1225	97.2	478	2 US-09-383-916-8	Sequence 8, Appl
44	1225	97.2	478	2 US-09-758-173-8	Sequence 8, Appl
45	1225	97.2	478	2 US-09-576-424-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5915824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-043A-50

Query Match 97.2%; Score 1225; DB 1; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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Db 1 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYDGVGVHVNKTPREEQNSTYRVVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT 120
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Qy 121 ISKAKVQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 180
Db 121 ISKAKGQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 181 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

RESULT 2
US-09-968-362A-26
; Sequence 26, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-26

Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116; Mismatches 4; Indels 0; Gaps 0;
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Qy 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Qy 121 ISKAKVQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 180
Db 121 ISKAKGQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 181 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

RESULT 3
US-09-932-812A-26
; Sequence 26, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-932-812A-26

Qy 121 ISKAKVQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 180
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Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 181 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

RESULT 3
US-09-932-812A-26
; Sequence 26, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-932-812A-26
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Best Local Similarity 97.0%; Pred. No. 3.5e-116; Mismatches 4; Indels 0; Gaps 0;
Matches 225; Conservative 3;

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Db 121 ISKAKGQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 180
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Db 181 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

RESULT 4
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hamman, Joseph P
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116; Mismatches 4; Indels 0; Gaps 0;
Matches 225; Conservative 3;

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Qy 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 160 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 219
Qy 121 ISKAKVQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 180
Db 220 ISKAKGQPREQVYTLPPSRDELTKQVSLTCLVKGYPDSIDIAVEWESNGQPENNYKTTT 279
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 280 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 331

RESULT 5
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
```

APPLICANT: Hamhang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/178,869
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-761-413-2

Query Match 97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 100 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
DB 160 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 219
QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180
DB 220 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 279
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
DB 280 PVLDSGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 331

RESULT 6
US-09-180-100-11
Sequence 11, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKAMURA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-100-11

Query Match 97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 129 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
DB 189 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 248
QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180
DB 249 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 308

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
DB 309 PVLDSGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 360
RESULT 7
US-09-949-713-11
Sequence 11, Application US/09949713
Patent No. 6953847
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6953847io
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/949,713
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/180,100
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-949-713-11

Query Match 97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 129 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
DB 189 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 248
QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180
DB 249 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 308
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
DB 309 PVLDSGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 360

RESULT 8
US-08-236-311-7
Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311

```
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Haseak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444PIC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-236-311-7

Query Match          97.2%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116; Indels 0; Gaps 0;
Matches 225; Conservative 3; Mismatches 4;

Qy 1 EPKSCDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 200 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 319
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 232
Db 320 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918

; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PIC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-457-918-7

Query Match          97.2%; Score 1225; DB 2; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116; Indels 0; Gaps 0;
Matches 225; Conservative 3; Mismatches 4;

Qy 1 EPKSCDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 200 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 319
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 232
Db 320 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 371

RESULT 10
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444PIC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7

Query Match 97.2%; Score 1225; DB 2; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 140 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199

QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 200 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 260 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 319

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
DB 320 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 371

RESULT 11
US-09-180-100-22
Sequence 22, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
PRIOR FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 376
TYPE: PRT
ORGANISM: Homo sapiens
US-09-949-713-22

Query Match 97.2%; Score 1225; DB 2; Length 376;
Best Local Similarity 97.0%; Pred. No. 7.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 145 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204

QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 205 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 265 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 324

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
DB 325 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 376

RESULT 12
US-09-949-713-22
Sequence 22, Application US/09949713
Patent No. 6953847
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6953847io
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/949,713
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/180,100
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 376
TYPE: PRT
ORGANISM: Homo sapiens
US-09-949-713-22

Query Match 97.2%; Score 1225; DB 2; Length 376;
Best Local Similarity 97.0%; Pred. No. 7.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 145 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204

QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 205 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 265 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 324

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
DB 325 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 376

RESULT 13
US-10-679-999-9
Sequence 9, Application US/10679999
Patent No. 6936439
GENERAL INFORMATION:

APPLICANT: Mann, Michael B.
APPLICANT: Hecht, Randy I.
TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/679,999
FILING DATE: 06-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/568,528
FILING DATE: 09-May-2000
APPLICATION NUMBER: 09/267,517
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W.
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-416
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1
OTHER INFORMATION: /note="Met (ATG) starts at -1"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-679-999-9

Query Match 97.2%; Score 1225; DB 2; Length 379;
Best Local Similarity 97.0%; Pred. No. 7.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 2 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 61
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKKVSNNKALPAPIEKT 120
DB 62 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKT 121
QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 122 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 181
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQOQSLSLSPGK 232
DB 182 PVLDSGDSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 233

RESULT 14

US-08-784-512-3
; Sequence 3, Application US/08784512
; Patent No. 5872209
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BUETTNER, Frank

APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggregan to study the proteolytic activity of
TITLE OF INVENTION: "Aggrecanase" in cell culture systems
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396
US-08-784-512-3
Query Match 97.2%; Score 1225; DB 1; Length 396;
Best Local Similarity 97.0%; Pred. No. 7.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 165 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 224
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKKVSNNKALPAPIEKT 120
DB 225 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKT 284
QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 285 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 344
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQOQSLSLSPGK 232
DB 345 PVLDSGDSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 396
RESULT 15
US-09-176-228-3
; Sequence 3, Application US/09176228
; Patent No. 6180334
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BUETTNER, Frank
; APPLICANT: CATERSON, Bruce


```

; APPLICANT: HUGHES, Clare
; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
; TITLE OF INVENTION: and native aggregran to study the proteolytic activity of
; TITLE OF INVENTION: "Aggregranase" in cell culture systems
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/176,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,512
; FILING DATE: 17-JAN-1997
; APPLICATION NUMBER: EP 96100682.2
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..396
;
US-09-176-228-3

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Query Match          97.2%; Score 1225; DB 2; Length 396;
Best Local Similarity 97.0%; Pred. No. 7.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 165 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224
QY 61 NMYVDGVEVHNKTKRREQYNSTYRVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKT 120
DB 225 NMYVDGVEVHNKTKRREQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 284
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 285 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 344
QY 181 PVLDSVGSFPLYSKLTVDKSRQQQGNVFCSVNHEALHNHYOQRSLSLSPGK 232
DB 345 PVLDSVGSFPLYSKLTVDKSRQQQGNVFCSVNHEALHNHYTKSLSLSPGK 396

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Search completed: February 22, 2006, 21:39:49
Job time : 35.4594 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:57:24 ; Search time 118.604 Seconds
(without alignments)
817.308 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQOQSLSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap:*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260	100.0	232	3	US-09-847-208-3
2	1260	100.0	232	4	US-10-000-439-3
3	1260	100.0	330	3	US-09-847-208-2
4	1260	100.0	330	4	US-10-000-439-2
5	1260	100.0	569	3	US-09-847-208-7
6	1260	100.0	569	4	US-10-000-439-7
7	1228	97.5	330	5	US-10-966-673-29
8	1225	97.2	232	3	US-09-996-357-10
9	1225	97.2	232	3	US-09-389-782-1
10	1225	97.2	232	4	US-10-617-619-7
11	1225	97.2	232	4	US-10-761-593A-26
12	1225	97.2	232	5	US-10-831-622-97
13	1225	97.2	232	5	US-10-800-497-26
14	1225	97.2	232	5	US-10-800-449-26
15	1225	97.2	232	5	US-10-964-215-97
16	1225	97.2	232	6	US-11-016-518A-26
17	1225	97.2	232	6	US-11-017-185-26
18	1225	97.2	234	5	US-10-627-556-684
19	1225	97.2	235	4	US-10-207-655-208
20	1225	97.2	235	5	US-10-627-556-2
21	1225	97.2	235	5	US-10-734-661A-6
22	1225	97.2	247	3	US-09-996-357-13
23	1225	97.2	251	4	US-10-008-063-18
24	1225	97.2	251	4	US-10-152-363A-6
25	1225	97.2	267	3	US-09-996-357-12
26	1225	97.2	269	5	US-10-609-783B-50
27	1225	97.2	285	6	US-11-018-102-11

28	1225	97.2	288	3	US-09-822-851B-14	Sequence 14, Appl
29	1225	97.2	288	4	US-10-119-637A-14	Sequence 14, Appl
30	1225	97.2	288	6	US-11-018-102-1	Sequence 1, Appl
31	1225	97.2	288	6	US-11-129-083-14	Sequence 14, Appl
32	1225	97.2	288	6	US-11-128-495-14	Sequence 14, Appl
33	1225	97.2	288	6	US-11-128-496-14	Sequence 14, Appl
34	1225	97.2	288	6	US-11-129-080-14	Sequence 14, Appl
35	1225	97.2	288	6	US-11-128-709-14	Sequence 14, Appl
36	1225	97.2	329	4	US-10-370-749-48	Sequence 37, Appl
37	1225	97.2	329	5	US-10-798-380-37	Sequence 37, Appl
38	1225	97.2	330	3	US-09-995-898A-15	Sequence 15, Appl
39	1225	97.2	330	3	US-09-892-949-38	Sequence 38, Appl
40	1225	97.2	330	4	US-10-047-542-20	Sequence 20, Appl
41	1225	97.2	330	4	US-10-269-805-68	Sequence 68, Appl
42	1225	97.2	330	4	US-10-310-719-8	Sequence 8, Appl
43	1225	97.2	330	4	US-10-112-582-1	Sequence 1, Appl
44	1225	97.2	330	4	US-10-320-231A-81	Sequence 81, Appl
45	1225	97.2	330	4	US-10-383-902A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-847-208-3
; Sequence 3, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UCG7.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-3

Query Match	100.0%	Score 1260;	DB 3;	Length 232;
Best Local Similarity	100.0%	Pred. No. 1.1e-92;		
Matches 232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	
Db	1	EPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	
QY	61	NYVDGVEVHNKTPREEQYNSTYRVVSVLTTLHQNMMNGKEYCKVSNKALPAPIEKT	120	
Db	61	NYVDGVEVHNKTPREEQYNSTYRVVSVLTTLHQNMMNGKEYCKVSNKALPAPIEKT	120	
QY	121	TSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180	
Db	121	TSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180	
QY	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNHYQOQSLSLSPGK	232	
Db	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNHYQOQSLSLSPGK	232	

RESULT 2

US-10-000-439-3
; Sequence 3, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES

```
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000.439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-3

Query Match      100.0%; Score 1260; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKKVSNNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKKVSNNKALPAPIEKT 120
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Qy 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 3
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match      100.0%; Score 1260; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKKVSNNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKKVSNNKALPAPIEKT 218
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 278
Qy 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
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Db 279 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 4
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000.439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match      100.0%; Score 1260; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKKVSNNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKKVSNNKALPAPIEKT 218
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 278
Qy 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 279 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 5
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
; OTHER INFORMATION: (IGe)
US-09-847-208-7

Query Match      100.0%; Score 1260; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 DB 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 6
 US-10-000-439-7
 ; Sequence 7, Application US/10000439
 ; Publication No. US20030064063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saxon, Andrew
 ; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
 ; FILE REFERENCE: UC067.004A
 ; CURRENT APPLICATION NUMBER: US/10/000,439
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: US 09/847,208
 ; PRIOR FILING DATE: 2001-05-01
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3
 ; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence
 US-10-000-439-7

Query Match 100.0%; Score 1260; DB 4; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3.2e-92;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 DB 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 7
 US-10-966-673-29
 ; Sequence 29, Application US/10966673
 ; Publication No. US20050226864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Protein Design Labs, Inc.
 ; APPLICANT: Hinton, Paul R
 ; APPLICANT: Tsurushita, Naoya
 ; TITLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
 ; FILE REFERENCE: 05882.0039.NPUS07
 ; CURRENT APPLICATION NUMBER: US/10/966,673

; CURRENT FILING DATE: 2004-10-15
 ; PRIOR APPLICATION NUMBER: US 60/562,627
 ; PRIOR FILING DATE: 2004-04-14
 ; PRIOR APPLICATION NUMBER: US 60/511,687
 ; PRIOR FILING DATE: 2003-10-15
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 29
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-10-966-673-29

Query Match 97.5%; Score 1228; DB 5; Length 330;
 Best Local Similarity 97.4%; Pred. No. 6.1e-90;
 Matches 226; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
 DB 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 218
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 DB 219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
 QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 DB 279 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 8
 US-09-996-357-10
 ; Sequence 10, Application US/09996357
 ; Patent No. US20020133001A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geffer, Malcolm L
 ; APPLICANT: Isreal, David I
 ; APPLICANT: Joyal, John L
 ; APPLICANT: Gosselin, Michael
 ; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
 ; TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
 ; FILE REFERENCE: PFI-105
 ; CURRENT APPLICATION NUMBER: US/09/996,357
 ; CURRENT FILING DATE: 2001-11-27
 ; PRIOR APPLICATION NUMBER: 60/253,302
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/250,198
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/257,186
 ; PRIOR FILING DATE: 2000-12-20
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-996-357-10

Query Match 97.2%; Score 1225; DB 3; Length 232;
 Best Local Similarity 97.0%; Pred. No. 7.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120


```

; APPLICANT: Wilkinson, Beverly
; TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: TSRI 810.1
; CURRENT APPLICATION NUMBER: US/10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-622-97

Query Match          97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 13
US-10-800-497-26
; Sequence 26, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; TITLE OF INVENTION: stimulating factor with
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-10-800-497-26

Query Match          97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 14
US-10-800-449-26
; Sequence 26, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-10-800-449-26

Query Match          97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 15
US-10-964-215-97
; Sequence 97, Application US/10964215
; Publication No. US20050152893A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
; TITLE OF INVENTION: OF TRANSPLANT REJECTION
; FILE REFERENCE: TSRI 810.2
; CURRENT APPLICATION NUMBER: US/10/964,215
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens

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DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 14
US-10-800-449-26
; Sequence 26, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-10-800-449-26

Query Match          97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 15
US-10-964-215-97
; Sequence 97, Application US/10964215
; Publication No. US20050152893A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
; TITLE OF INVENTION: OF TRANSPLANT REJECTION
; FILE REFERENCE: TSRI 810.2
; CURRENT APPLICATION NUMBER: US/10/964,215
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-964-215-97

Query Match	97.2%	Score 1225;	DB 5;	Length 232;
Best Local Similarity	97.0%	Pred. No. 7.1e-90;		
Matches 225;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	1	EPKSCDKHTHTCP	PAPELLGGPSVFL	PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Db	1	EPKSCDKHTHTCP	PAPELLGGPSVFL	PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Qy	61	NWYVDGVEVHNKTKPREEQYNSTYRV	SVLT	TVLHQNMNMGKEYCKKVS	NKALPAPIEKT 120
Db	61	NWYVDGVEVHNKTKPREEQYNSTYRV	SVLT	TVLHQDNLNGKEYCKKVS	NKALPAPIEKT 120
Qy	121	ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSP	SDIAVEWESNGQPENNYKTTP	180	
Db	121	ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSP	SDIAVEWESNGQPENNYKTTP	180	
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNV	FSCVMHEALHNHYTQKSLSLSPGK	232	
Db	181	PVLDSVGSFFLYSKLTVDKSRWQQGNV	FSCVMHEALHNHYTQKSLSLSPGK	232	

Search completed: February 22, 2006, 22:03:09
Job time : 119.604 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:58:19 ; Search time 12.0207 Seconds
(without alignments)
287.324 Million cell updates/sec

Title: US-10-000-439-3
Perfect score: 1260
Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQRRLSLSFGK 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
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8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	232	6	US-10-948-053-1
2	1225	97.2	232	7	US-11-227-340-7
3	1225	97.2	251	7	US-11-242-294-6
4	1225	97.2	330	6	US-10-886-383-6
5	1225	97.2	330	6	US-10-493-909-20
6	1225	97.2	330	6	US-10-982-440-68
7	1225	97.2	330	7	US-11-022-289-11
8	1225	97.2	330	7	US-11-075-351-1
9	1225	97.2	330	7	US-11-165-141-15
10	1225	97.2	330	7	US-11-102-621-3
11	1225	97.2	330	7	US-11-102-621-7
12	1225	97.2	330	7	US-11-005-726-164
13	1225	97.2	330	7	US-11-124-620-1
14	1225	97.2	330	7	US-11-233-683-1
15	1225	97.2	335	7	US-11-024-251-35
16	1225	97.2	444	7	US-11-172-320-6
17	1225	97.2	444	7	US-11-173-969-6
18	1225	97.2	450	7	US-11-005-726-161
19	1225	97.2	450	7	US-11-049-536-701
20	1225	97.2	451	7	US-11-158-505-33
21	1225	97.2	451	7	US-11-124-620-7
22	1225	97.2	452	7	US-11-016-503-6
23	1225	97.2	459	6	US-10-949-720-390
24	1225	97.2	462	7	US-11-016-503-8
25	1225	97.2	470	7	US-11-072-512-3730

26	1225	97.2	476	7	US-11-139-499-4	Sequence 4, Appli
27	1225	97.2	476	7	US-11-139-499-12	Sequence 12, Appli
28	1225	97.2	478	7	US-11-139-499-8	Sequence 8, Appli
29	1225	97.2	551	7	US-11-022-289-7	Sequence 8, Appli
30	1225	97.2	551	7	US-11-022-289-8	Sequence 8, Appli
31	1225	97.2	557	7	US-11-016-503-4	Sequence 4, Appli
32	1225	97.2	557	7	US-11-022-289-4	Sequence 4, Appli
33	1225	97.2	557	7	US-11-022-289-5	Sequence 5, Appli
34	1225	97.2	557	7	US-11-022-289-6	Sequence 6, Appli
35	1225	97.2	567	7	US-11-016-503-2	Sequence 2, Appli
36	1225	97.2	567	7	US-11-016-503-10	Sequence 10, Appli
37	1225	97.2	641	7	US-11-227-340-8	Sequence 8, Appli
38	1225	97.2	679	7	US-11-227-340-11	Sequence 11, Appli
39	1225	97.2	701	7	US-11-227-340-6	Sequence 6, Appli
40	1225	97.2	771	6	US-10-949-720-389	Sequence 389, App
41	1223	97.1	592	6	US-10-016-686-4	Sequence 4, Appli
42	1222	97.0	330	7	US-11-102-621-71	Sequence 71, Appli
43	1222	97.0	446	7	US-11-102-621-121	Sequence 121, App
44	1222	97.0	447	7	US-11-102-621-132	Sequence 132, App
45	1220	96.8	330	7	US-11-102-621-70	Sequence 70, Appli

ALIGNMENTS

RESULT 1
US-10-948-053-1
; Sequence 1, Application US/10948053
; Publication No. US20060019887A1
; GENERAL INFORMATION:
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: Compositions and Methods for the Prevention or Treatment of Canc
; TITLE OF INVENTION: Bone Loss Associated with Cancer
; FILE REFERENCE: A-605
; CURRENT APPLICATION NUMBER: US/10/948,053
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/389,545
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-053-1

Query Match	97.2%	Score 1225;	DB 6;	Length 232;
Best Local Similarity	97.0%;	Pred. No. 1.7e-101;		
Matches 225;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	EPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
Db	1	EPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
Qy	61	NWYDGVGVHNVKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT	120	
Db	61	NWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT	120	
Qy	121	ISKAVQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180	
Db	121	ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180	
Qy	181	PVLDSGVGFYLYSKLTVDKSRWQQGNVSCSVMHEALHNHYQRRLSLSLSPGK	232	
Db	181	PVLDSGVGFYLYSKLTVDKSRWQQGNVSCSVMHEALHNHYQRRLSLSLSPGK	232	

RESULT 2
US-11-227-340-7
; Sequence 7, Application US/11227340
; Publication No. US20060024730A1
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soren E

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; APPLICANT: Nicolaisen, Else M
; APPLICANT: Jorgensen, Anker S
; TITLE OF INVENTION: TF Binding Compound
; FILE REFERENCE: 6455.200-US
; CURRENT APPLICATION NUMBER: US/11/227,340
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/10/617,619
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,568
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human
US-11-227-340-7

Query Match          97.2%; Score 1225; DB 7; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.7e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
Db 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232

RESULT 3
US-11-242-294-6
; Sequence 6, Application US/11242294
; Publication No. US20060034852A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TAC1-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/11/242,294
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/10/152,363
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-242-294-6

Query Match          97.2%; Score 1225; DB 7; Length 251;
Best Local Similarity 97.0%; Pred. No. 1.9e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 20 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 79
Qy 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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Db 80 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 139
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Db 140 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 199
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
Db 200 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 251

RESULT 4
US-10-886-383-6
; Sequence 6, Application US/10886383
; Publication No. US20060005571A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and use:
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,383
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-383-6

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158

Qy 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 159 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
Db 279 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 330

RESULT 5
US-10-493-909-20
; Sequence 20, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493,909
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
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; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-20

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 232
DB 279 PVLDSGSPFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
```

```
RESULT 6
US-10-982-440-68
; Sequence 68, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-68

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 232
DB 279 PVLDSGSPFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
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```
RESULT 7
US-11-022-289-11
; Sequence 11, Application US/1102289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 11
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-289-11

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 232
DB 279 PVLDSGSPFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
```

```
RESULT 8
US-11-075-351-1
; Sequence 1, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-1

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 232
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```
RESULT 12
US-11-005-726-164
; Sequence 164, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLEDOORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566
; PRIOR FILING DATE: 2002-11-11
; PRIOR APPLICATION NUMBER: EP 01126858.8
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain
; OTHER INFORMATION: constant region
US-11-005-726-164

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
   |||||
Db 99 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 158

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIEKT 120
   |||||
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 218

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDVSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 232
   |||||
Db 279 PVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 330

RESULT 13
US-11-124-620-1
; Sequence 1, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
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; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-620-1

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
   |||||
Db 99 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 158

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIEKT 120
   |||||
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 218

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDVSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 232
   |||||
Db 279 PVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 330

RESULT 14
US-11-233-683-1
; Sequence 1, Application US/11233683
; Publication No. US20060025573A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/11/233,683
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-11-233-683-1

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
   |||||
Db 99 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 158

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIEKT 120
   |||||
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 218
```

```
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232
Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKLSLSLSPGK 330

RESULT 15
US-11-024-251-35
; Sequence 35, Application US/11024251
; Publication No. US20050266425A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Paris, Mark
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
; FILE REFERENCE: 1843.0230001
; CURRENT APPLICATION NUMBER: US/11/024,251
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: 60/533,241
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: IgG Secreted Constant Domain
US-11-024-251-35

Query Match 97.2%; Score 1225; DB 7; Length 335;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 104 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 163
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVQLHQNMGKEYCKVSNKALPAPIEKT 120
Db 164 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVQLHQNMGKEYCKVSNKALPAPIEKT 223
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 224 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 283
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232
Db 284 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKLSLSLSPGK 335

Search completed: February 22, 2006, 22:03:44
Job time : 12.0207 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:11 ; Search time 152.263 Seconds
(without alignments)
669.475 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPEL.....MHEALTHYQRRSLSPCK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1260	100.0	232	6 AAO19665	Aao19665 Human Igg
2	1260	100.0	330	6 AAO19664	Aao19664 Human Igg
3	1260	100.0	569	6 AAO19668	Aao19668 GR2 fusio
4	1232	97.8	232	9 AD287506	Adz87506 Human Igg
5	1228	97.5	330	9 ADz89628	Adz89628 Human Igg
6	1225	97.2	232	2 AAW26232	Aaw26232 Human Igg
7	1225	97.2	232	3 AAB28690	Aab28690 Human Igg
8	1225	97.2	232	4 AAB80897	Aab80897 Human Igg
9	1225	97.2	232	4 AAY72915	Aay72915 Human par
10	1225	97.2	232	5 AAE15347	Aae15347 Human imm
11	1225	97.2	232	5 AAE26272	Aae26272 Human Igg
12	1225	97.2	232	7 ADJ65991	Adj65991 Herpes vl
13	1225	97.2	232	8 ADJ57512	Adj57512 Human Igg
14	1225	97.2	232	8 ADz48992	Adz48992 Human Igg
15	1225	97.2	232	8 ADU51146	Adu51146 Human spl
16	1225	97.2	232	8 ADW39127	Adw39127 Novel TNP
17	1225	97.2	232	9 ADV91799	Adv91799 Human GCS
18	1225	97.2	232	9 ADV99720	Adv99720 Human Igg
19	1225	97.2	232	9 ADY55884	Ady55884 Human Igg
20	1225	97.2	232	9 ADz86538	Adz86538 Human Igg
21	1225	97.2	232	9 AEa18941	Aea18941 Human Igg
22	1225	97.2	232	9 AEa88761	Aea88761 Human Igg
23	1225	97.2	233	5 ABb09463	Abb09463 Human Igg
24	1225	97.2	234	5 ADy22146	Ady22146 Human imm

25	1225	97.2	235	6 ABJ38647	Abj38647 pCXFc pro
26	1225	97.2	235	6 ADA89055	Ada89055 Plasmid p
27	1225	97.2	235	7 ADD25647	Add25647 Binding d
28	1225	97.2	235	7 ADG74307	Adg74307 Fibroblas
29	1225	97.2	235	9 ADY21627	Ady21627 Human Igg
30	1225	97.2	247	5 AAE26274	Aae26274 Human bet
31	1225	97.2	251	5 ABB81490	Abb81490 Human imm
32	1225	97.2	251	6 AAE35214	Aae35214 Human wil
33	1225	97.2	259	2 AAY24154	Aay24154 Protein f
34	1225	97.2	267	5 AAE26273	Aae26273 Human tpa
35	1225	97.2	269	8 ADJ52120	Adj52120 CH1 delet
36	1225	97.2	285	9 AEA89551	Aea89551 Human imm
37	1225	97.2	287	4 AAB47590	Aab47590 Fusion pr
38	1225	97.2	288	9 AEA89541	Aea89541 Human imm
39	1225	97.2	329	2 AAR91806	Aar91806 Human imm
40	1225	97.2	329	8 ADP56389	Adp56389 Human PRO
41	1225	97.2	329	8 ADS82579	Ads82579 Human Igg
42	1225	97.2	330	4 AAB04071	Aab04071 Zcytor 10
43	1225	97.2	330	5 AAM47856	Aam47856 Human Ig-
44	1225	97.2	330	5 AAE21960	Aae21960 Human dea
45	1225	97.2	330	5 ABB81641	Abb81641 Human Igg

ALIGNMENTS

RESULT 1

AAO19665
ID AAO19665 standard; protein; 232 AA.

XX AAO19665;

XX 28-MAR-2003 (first entry)

XX Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.

XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
XX Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
XX antiasthmatic; antiallergic; antiinflammatory; dermatological;
XX antiarthritic; antirheumatic; antidiabetic; neuroprotective;
XX hinge-CH2-CH3 region.

XX Homo sapiens.

XX WO200288317-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013527.

XX 01-MAY-2001; 2001US-00847208.

XX 24-OCT-2001; 2001US-00000439.

XX (REGC) UNIV CALIFORNIA.

XX Saxon A, Zhang K, Zhu D;

XX WPI; 2003-103456/09.

XX New fusion molecules comprising polypeptide sequences that bind to IgG
XX inhibitory receptor and native IGE receptor, useful for treating IGE-
XX mediated hypersensitivity reactions, e.g. asthma or allergies, or
XX autoimmune diseases.

XX Claim 19; Fig 3; 116pp; English.

XX The present invention relates to a fusion molecule comprising a first
XX polypeptide sequence capable of specific binding to a native Igg
XX inhibitory receptor consisting of an immune receptor tyrosine-based
XX inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
XX functionally connected to a second polypeptide sequence capable of
XX specific binding directly or indirectly to a native IGE receptor
XX (FcepsilonR). Also provided are nucleotide sequences encoding such a

CC fusion protein. The fusion molecules and compositions are useful for
 CC treating an IGE-mediated biological response, preferably an IGE-mediated
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
 CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
 CC or symptoms resulting from, a type I hypersensitivity reaction in a
 CC subject receiving immunotherapy. The present sequence is the human IgG1
 CC heavy chain constant region hinge-CH2-CH3 portion
 XX

SQ Sequence 232 AA;
 Query Match 100.0%; Score 1260; DB 6; Length 232;
 Best Local Similarity 100.0%; Pred. No. 3.3e-91;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSPGK 232
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSPGK 232

RESULT 2
 AAO19664
 ID AAO19664 standard; protein; 330 AA.
 XX
 AC AAO19664;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Human IgG1 heavy chain constant region.
 XX

Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 FN WO200288317-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 XX
 PR 01-MAY-2001; 2001US-00847208.
 XX
 PR 24-OCT-2001; 2001US-00000439.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX

Saxon A, Zhang K, Zhu D;
 FI WPI; 2003-103456/09.
 DR
 PT New fusion molecules comprising polypeptide sequences that bind to IgG
 PT inhibitory receptor and native IGE receptor, useful for treating IGE-
 PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
 PT autoimmune diseases.
 XX
 PS Claim 64; Fig 2; 116pp; English.
 XX
 CC The present invention relates to a fusion molecule comprising a first

CC polypeptide sequence capable of specific binding to a native IgG
 CC inhibitory receptor consisting of an immune receptor tyrosine-based
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
 CC functionally connected to a second polypeptide sequence capable of
 CC specific binding directly or indirectly to a native IGE receptor
 CC (Fc epsilonR). Also provided are nucleotide sequences encoding such a
 CC fusion protein. The fusion molecules and compositions are useful for
 CC treating an IGE-mediated biological response, preferably an IGE-mediated
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
 CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
 CC or symptoms resulting from, a type I hypersensitivity reaction in a
 CC subject receiving immunotherapy. The present sequence is the human IgG1
 CC heavy chain constant region
 XX

SQ Sequence 330 AA;
 Query Match 100.0%; Score 1260; DB 6; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5.1e-91;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
 DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 218
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 180
 DB 219 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 278
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSPGK 232
 DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSPGK 330

RESULT 3
 AAO19668
 ID AAO19668 standard; protein; 569 AA.
 XX
 AC AAO19668;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE GE2 fusion protein for use in treating immune diseases.
 XX

Human; IgG; immunoglobulin E; immunotherapy; immune disease;
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2;
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FN WO200288317-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 XX
 PR 01-MAY-2001; 2001US-00847208.
 XX
 PR 24-OCT-2001; 2001US-00000439.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX

Saxon A, Zhang K, Zhu D;
 FI WPI; 2003-103456/09.
 DR
 PT New fusion molecules comprising polypeptide sequences that bind to IgG
 PT inhibitory receptor and native IGE receptor, useful for treating IGE-
 PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
 PT autoimmune diseases.
 XX
 PS Claim 64; Fig 2; 116pp; English.
 XX
 CC The present invention relates to a fusion molecule comprising a first

PT New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IGE receptor, useful for treating Ige-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX
PS Claim 35; Fig 7; 116pp; English.
XX
CC The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IGE receptor
CC (FcεpsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC treating an Ige-mediated biological response, preferably an Ige-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is a gammahinge-
CC CHgamma2-CHgamma3-(Gly4Ser)3-Chepsilon2-Chepsilon3 fusion
CC protein (designated G52) of the invention
XX
SQ Sequence 569 AA;
Query Match 100.0%; Score 1260; DB 6; Length 569;
Best Local Similarity 100.0%; Pred. No. 9.7e-91;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHNMMNGKEYCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHNMMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
RESULT 4
ADZ87506
ID ADZ87506 standard; protein; 232 AA.
XX
AC ADZ87506;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human IgG1 protein region SeqID33.
XX
KW protein engineering; immunoglobulin; cytostatic; cancer.
XX
OS Homo sapiens.
XX
PN WO2005042573-A1.
XX
PD 12-MAY-2005.
XX
PF 21-OCT-2004; 2004WO-US034680.
XX
PR 24-OCT-2003; 2003US-0514198P.
XX
PR 12-NOV-2003; 2003US-0519822P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (ILEX-) ILEX PROD INC.

XX Kharbanda S, Kufe DW;
XX WPI: 2005-346855/35.
DR N-PSDB; ADZ87507.
XX
PT MUC1 ligand trap comprising a MUC1 extracellular polypeptide and an
PT immunoglobulin FC polypeptide or an albumin polypeptide, useful for
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 33; 82pp; English.
XX
CC This invention relates to a novel MUC1 chimeric protein which comprises a
CC first polypeptide sequence and a second polypeptide sequence, where the
CC first polypeptide sequence is a MUC1 extracellular (MUC1-EC) polypeptide,
CC and the second polypeptide sequence is a human immunoglobulin FC
CC polypeptide or a human albumin polypeptide. The invention may be useful
CC for the development of compounds with a cytostatic activity acting as
CC MUC1 antagonists or CD227 antagonists. The MUC1 chimeric protein is
CC useful in preparing a composition for treating cancer. The present
CC sequence is that of a protein which was used during the development of
CC the novel MUC1 chimeric protein of the invention.
XX
SQ Sequence 232 AA;
Query Match 97.8%; Score 1232; DB 9; Length 232;
Best Local Similarity 97.4%; Pred. No. 5.4e-89;
Matches 226; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHNMMNGKEYCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHNMMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
RESULT 5
ADZ69628
ID ADZ69628 standard; protein; 330 AA.
XX
AC ADZ69628;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human IgG1 heavy chain constant region, mutant L314M.
XX
KW Heavy chain constant region; antibody engineering; protein engineering;
KW immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasm;
KW autoimmune disease; immunosuppressive; immune disorder.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 197 /note= "Wild-type Leu substituted by Met"
XX
PN WO2005037867-A1.
XX
PD 28-APR-2005.
XX
PF 15-OCT-2004; 2004WO-US034440.
XX

PR 15-OCT-2003; 2003US-0511687P.
 PR 14-APR-2004; 2004US-0562627P.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX Hinton PR, Teurushita N;
 PI WPI; 2005-315683/32.

XX New modified Fc-fusion protein where at least one amino acid residue from
 PT the heavy chain constant region, useful for studying protein function in
 PT vitro and in vivo and as potential therapeutic and diagnostic agents.
 XX
 PS Claim 21; SEQ ID NO 29; 170pp; English.

CC The invention relates to a modified Fc-fusion protein where at least one
 CC amino acid residue from the heavy chain constant region selected from
 CC residues 250, 314, and 428 (Kabat numbering) is different from that
 CC present in the unmodified Fc-fusion protein. Also included are an Fc-
 CC fusion protein comprising an Fc region substantially identical to that of
 CC a naturally occurring class IgG antibody, a modified Fc-fusion protein
 CC with an in vivo mean elimination half-life at least about 1.3-fold longer
 CC than that of the corresponding unmodified Fc-fusion protein, a modified
 CC IgG class antibody fragment (comprising a heavy chain constant region or
 CC Fc-region where at least one amino acid residue selected from the group
 CC consisting of residues 250, 314, and 428 is different from that present
 CC in the unmodified IgG class antibody), an isolated polynucleotide
 CC molecule encoding a polypeptide comprising a sequence at least 90%
 CC identical to a sequence selected from AD269600-AD269656, an isolated
 CC polypeptide comprising an amino acid sequence at least 90% identical to a
 CC sequence selected from AD269600-AD269656, a method for altering FcRn
 CC binding affinity/serum half-life of an Fc-fusion protein (comprising
 CC selecting at least one amino acid residue as cited above, and
 CC substituting the selected residue(s) with an amino acid different from
 CC that present in the Fc-fusion protein) and a method of producing a
 CC modified Fc-fusion protein with an altered binding affinity for
 CC FcRn/alters serum half-life as compared with the unmodified Fc-fusion
 CC protein (comprising preparing an expression vector comprising a suitable
 CC promoter operably linked to DNA encoding at least a constant region of an
 CC IgG heavy chain, transforming host cells with the vector and culturing
 CC the transformed host cells to produce the modified IgG Fc fusion
 CC protein). The modified antibody has a higher affinity for FcRn at pH 6.0
 CC than at pH 8.0. The fusion proteins are useful for studying protein
 CC function in vitro and in vivo and as potential therapeutic and diagnostic
 CC agents. The present sequence represents a human IgG1 heavy chain constant
 CC region with an amino acid substitution at residue 250, 314 or 428 (Kabat
 CC numbering, the actual residue that is mutated is covered in the feature
 CC table).

XX SQ Sequence 330 AA;

Query Match 97.5%; Score 1228; DB 9; Length 330;
 Best Local Similarity 97.4%; Pred. No. 1.7e-88;
 Matches 226; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
 QY 61 NYYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKVKCKVSNKALPAPIEKT 120
 DB 159 NYYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKVKCKVSNKALPAPIEKT 218
 QY 121 ISKAKVQPREPVQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 DB 219 ISKAKGQPREPVQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
 QY 181 PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
 DB 279 PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 6

AAW26232
 ID AAW26232 standard; protein; 232 AA.

XX
 AC AAW26232;
 XX
 DT 16-MAR-1998 (first entry)
 XX
 DE Human IgG1 hinge/Fc region.
 XX
 KW Fusion protein; hydrophilic spacer; recombinant; expression system;
 KW carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.
 XX
 OS Homo sapiens.
 XX
 FN WO9728272-A1.

XX 07-AUG-1997.

XX 31-JAN-1997; 97WO-US001470.

XX 31-JAN-1996; 96US-00595043.

XX (TECH-) TECHNOLOGENE INC.

XX Sgarlato GD;

XX WPI; 1997-402624/37.

XX N-PSDB; AAT80158.

XX Recombinant protein expression system for fusion protein production -
 PT useful for high quantity production of authentic recombinant proteins.

XX Example 3; Page 133-134; 194pp; English.

XX A novel recombinant vector has been developed which comprises a
 CC nucleotide sequence encoding a fusion protein. The fusion protein
 CC comprises three domains joined together in order, from N-terminus to C-
 CC terminus, of a first domain comprising a protein of interest, a second
 CC domain comprising a hydrophilic spacer and an affinity domain, each
 CC domain comprising amino acid residues. The present sequence represents
 CC the hinge/Fc region of human IgG1, used in example 3 of the present
 CC invention. The recombinant vector is used for the production of authentic
 CC recombinant proteins of interest. The method of the invention is useful
 CC for the expression of fusion proteins capable of isolation by affinity
 CC chromatography in pro- or eukaryotic cells. This method allows for the
 CC efficient cleavage and generation of authentic proteins of interest that
 CC do not contain extraneous (i.e. non-naturally occurring) amino acids

XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 2; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NYYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKVKCKVSNKALPAPIEKT 120
 DB 61 NYYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKVKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPVQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 DB 121 ISKAKGQPREPVQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 QY 181 PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

RESULT 7

AAB28690

ID AAB28690 standard; protein; 232 AA.
 AC AAB28690;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Human IgGgamma hinge, CH2 and CH3 regions.
 XX
 XX Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
 KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 KW transplant rejection; cardiovascular disease; arteriosclerosis;
 KW IgGgamma.
 XX
 OS Homo sapiens.
 XX
 PN WO200063253-A1.
 XX
 PD 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US008004.
 PF
 XX 16-APR-1999; 99US-00293245.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Hsu H, Meng S;
 PI
 XX WPI; 2000-665240/64.
 DR
 XX Fusion protein of AGP-1 protein and an Fc region, used to treat
 PT proliferative disorders, immune disorders, and virally-induced disorders.
 PT
 XX Claim 2; Fig 1; 93pp; English.
 PS
 XX The present sequence was used in the production of AGP-1 fusion proteins.
 CC AGP-1 is a type II transmembrane protein. The fusion proteins comprise an
 CC Fc immunoglobulin region fused to the N-terminal portion of the AGP-1
 CC protein. The fusion proteins can be used to induce apoptosis in a tissue,
 CC and to treat proliferative disorders, immune disorders, or virally-
 CC induced disorders. The proliferative disorders include cancers, such as
 CC breast, prostate, lung or colon cancer. The viral infections include
 CC hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune
 CC disorders may be autoimmune disorders or transplant rejection.
 CC Cardiovascular diseases such as arteriosclerosis may also be treated. The
 CC AGP-1 containing fusion proteins have increased biological activity
 CC compared to the soluble AGP-1 proteins used in prior art therapies
 CC
 XX SQ Sequence 232 AA;
 Query Match 97.2%; Score 1225; DB 3; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
 DB 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 RESULT 8
 AAY72915

AAB80897
 ID AAB80897 standard; protein; 232 AA.
 XX
 AC AAB80897;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human IgGgamma hinge, CH2 and CH3 regions.
 XX
 XX Human; IgGgamma; anticancer; Antimetastatic; Osteogenic;
 KW lytic bone disease; multiple myeloma; immunoglobulin;
 KW osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition.
 XX
 OS Homo sapiens.
 XX
 PN WO200117543-A2.
 XX
 PD 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-US022806.
 PF
 XX 03-SEP-1999; 99US-00389545.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Dunstan CR;
 PI
 XX WPI; 2001-265936/27.
 DR
 XX Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
 PT
 XX Disclosure; Fig 1; 87pp; English.
 PS
 XX The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)
 CC polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-
 CC AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)
 CC by blocking differentiation from monocytes/macrophage precursors. The
 CC present sequence is the hinge, CH2 and CH3 regions of human IgGgamma.
 CC This sequence can be used to generate fusion proteins of OPG and
 CC immunoglobulin, for use in the present invention. The generated fusion
 CC proteins can exhibit increased circulating half-lives and slower
 CC clearance times, thereby providing a more sustained activity
 CC
 XX SQ Sequence 232 AA;
 Query Match 97.2%; Score 1225; DB 4; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
 DB 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 RESULT 9
 AAY72915

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTT 180
 DB 121 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTT 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKSLSLSPGK 232

RESULT 13
 ADJ57512
 ID ADJ57512 standard; protein; 232 AA.
 XX
 AC ADJ57512;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human IgG1 Fc domain fragment.
 XX
 KW TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;
 KW cerebroprotective; cytostatic; vasotropic; antirheumatic; antiarthritic;
 KW antiarteriosclerotic; antinflammatory; antibacterial; immunosuppressive;
 KW hypertensive; cardiant; coagulation Factor VII; human; immunoglobulin G1;
 KW IgG1.
 XX
 OS Homo sapiens.
 XX
 FN WO2004006962-A2.
 XX
 PD 22-JAN-2004.
 XX
 PF 09-JUL-2003; 2003WO-DK000481.
 XX
 PR 12-JUL-2002; 2002DK-00001099.
 XX
 PA (NOVO) NOVO NORDISK AS.
 FI Bjorn SE, Nicolaisen EM, Steenstrup TD;
 DR WPI; 2004-180224/17.
 XX
 PT New compound binding to tissue factor, useful for treating diseases such
 as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.
 XX
 PS Claim 16; SEQ ID NO 7; 61pp; English.
 XX

The invention relates to a compound (I) binding to tissue factor (TF).
 The compound (I) has the formula A-(LM)-C, where A is a FVIIa
 polypeptide, LM is an optional linker group, C comprises an
 immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-
 mediated activated factor VII (FVIIa) activity. (I) is useful as a
 medicament, and for the manufacture of a medicament for preventing or
 treating disease or disorder associated with pathophysiological TF
 activity. The disease or disorder associated with pathophysiological TF
 activity are deep venous thrombosis, arterial thrombosis, post surgical
 thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal
 coronary angioplasty (PTCA), stroke, cancer, tumor metastasis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicemia, hypotension,
 CC adult respiratory distress syndrome (ARDS), disseminated intravascular
 CC coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial
 CC infarction, or prophylactic treatment of mammals with atherosclerotic
 CC vessels at risk for thrombosis. The present sequence represents the Fc
 CC domain fragment of human immunoglobulin G1 (IgG1).
 XX
 SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60

DB 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKT 120
 DB 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTT 180
 DB 121 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTT 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKSLSLSPGK 232

RESULT 14
 ADR48992
 ID ADR48992 standard; peptide; 232 AA.
 XX
 AC ADR48992;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human IgG1 hinge and CH2 region.
 XX
 KW antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;
 KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
 KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
 XX
 OS Homo sapiens.
 XX
 FN US2004175824-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 21-JAN-2004; 2004US-00761593.
 XX
 PR 17-AUG-2001; 2001US-00932812.
 XX
 PA (SUNL/) SUN L K.
 PA (SUNB/) SUN B N C.
 PA (SUNC/) SUN C R Y.
 XX
 PI Sun LK, Sun BNC, Sun CRY;
 XX
 WPI; 2004-634851/61.
 XX
 PT New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
 (HuEPO), a peptide linker, and a human Igg Fc variant, useful for
 PT treating chronic anemia due to renal diseases, cancer chemotherapy, or
 PT rheumatoid arthritis.
 XX
 PS Disclosure; SEQ ID NO 26; 31pp; English.
 XX

A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
 (HuEPO), a peptide linker, and a human Igg Fc variant, is new.
 CC INDEPENDENT CLAIMS are also included for the following: a chinese hamster
 CC ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in
 CC its growth medium in excess of 10 microg per million cells in a 24 hour
 CC period; and a method for making a recombinant fusion protein comprising
 CC HuEPO, a flexible peptide linker, and a human Igg Fc variant. Preferred
 CC Protein: The peptide linker containing 20 or fewer amino acids is present
 CC between HuEPO and the human Igg Fc variant, and comprises two or more
 CC amino acids selected from glycine, serine, alanine, and threonine. The
 CC human Igg Fc variant comprises a hinge, CH2, and CH3 domains of human
 CC IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
 CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
 CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
 CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1
 CC with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino
 CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro
 CC biological activity similar to or higher than that of rHuEPO on a molar

CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line
 CC producing the HuEPO-L-vfc fusion protein in its growth medium in excess
 CC of 30 μ mol/g per million cells in a 24 hour period. The human IgG Fc
 CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from
 CC IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
 CC the IgG Fc contains amino acid mutations to attenuate effector functions,
 CC a flexible peptide linker containing 20 or fewer amino acids is present
 CC between HuEPO and human IgG Fc variant, and the HuEPO-L-vfc fusion
 CC protein exhibits in vitro biological activity similar to or higher than
 CC that of rHuEPO on a molar basis. Preferred Method: Making a recombinant
 CC fusion protein comprising HuEPO, a flexible peptide linker, and a human
 CC IgG Fc variant comprises: generating a CHO-derived cell line; growing the
 CC cell line where the recombinant protein is expressed in its growth medium
 CC in excess of 10 μ mol/g per million cells in a 24 hour period; and
 CC purifying the expressed protein from (b), where the recombinant fusion
 CC protein exhibits in vitro biological activity similar to or higher than
 CC that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological
 CC data given. None given. Administration can be through subcutaneous or
 CC intravenous route. No dosage given. The recombinant HuEPO-L-vfc fusion
 CC protein is useful for treating patients with chronic anemia due to renal
 CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for
 CC HIV infection, or myelodysplastic syndrome. It is also useful in the
 CC treatment of renal failure. A fusion protein was assembled from several
 CC DNA segments. To obtain the gene encoding the leader peptide and mature
 CC protein of human erythropoietin (EPO), cDNA library of human fetal liver
 CC or kidney was used as the template in polymerase chain reaction (PCR).
 CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a
 CC restriction enzyme cleavage site is used as the 5' oligonucleotide
 CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon
 CC and incorporates a BamHI site. The resulting DNA fragments of
 CC approximately 600 bp were inserted into a holding vector such as pUC19 at
 CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the
 CC human EPO gene was confirmed by DNA sequencing.

XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NWYDGVGVHVNKTTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 DB 61 NWYDGVGVHVNKTTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232

RESULT 15

ADU51146
 ID ADU51146 standard; protein; 232 AA.

XX ADU51146;

XX 27-JAN-2005 (first entry)

DE Human spleen-expressed receptor-related solubility-promoting protein.

XX immunosuppressive; cytostatic; antiinflammatory; immune modulation;
 KW intercellular communication; autoimmune disease; cancer; neoplasm;
 KW transplant rejection; immune disorder; inflammation; gene therapy.

OS Homo sapiens.

XX

PN WO2004096976-A2.
 XX 11-NOV-2004.
 XX 29-APR-2004; 2004WO-EP004562.
 XX 30-APR-2003; 2003US-0467206P.
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 PA (SCRI) SCRIPPS RES INST.
 XX Kaye J, Wilkinson B;
 PI WPI; 2004-804740/79.

XX New purified spleen expressed (SPFX) polypeptide useful for modulating
 PT lymphocyte activation and the immune response in disorders including
 PT autoimmunity, cancer, transplant rejection and inflammation.

XX Disclosure; SEQ ID NO 97; 98pp; English.

XX The invention relates to a novel purified polypeptide comprising any of
 CC SEQ ID NOS: 3, 7, 9, 11, 45 or 88, or an amino acid sequence that is 95%
 CC or more identical to the amino acid sequences and which includes an
 CC immunoglobulin like domain structure. The polypeptide of the invention
 CC demonstrates immunosuppressive, cytostatic and antiinflammatory
 CC activities and is a spleen-expressed (SPFX) polypeptide. The methods and
 CC compositions of the present invention may be useful for modulating
 CC lymphocyte activation and the immune response in a variety of conditions
 CC including autoimmunity, cancer, transplant rejection and inflammation.
 CC Such modulation may be achieved via the use of gene therapy. The current
 CC sequence is that of the human spleen-expressed (SPFX) receptor-related
 CC solubility-promoting protein of the invention.

XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NWYDGVGVHVNKTTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 DB 61 NWYDGVGVHVNKTTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232

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 Job time : 155.263 secs

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